STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number

TO: Sarvamangala Devi
Art Unit: 1645
Location: REM 3C18
Serial Number: 10/054536

Tuesday, June 21, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

157124

From:	Devi, Sarvamangala
Sent:	Friday, June 17, 2005 7:42 AM
To:	Shears, Beverly
Subject:	10/054,536

Beverly:

In application 10/054,536, please perform a sequence search for SEQ ID NO: 2 in commercial and pending databases.

Thanx.

S. DEVI, Ph.D.
AU 1645
Rems - 3C18

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1

Date completed: _____

Searcher: _Beverly e 2528_

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

__✓__ Other CGN

PTO-1590 (9-90)

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          GenCore version 5.1.6
     Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    June 19, 2005, 15:45:05 ; Search time 3604 Seconds
                     (without alignments)
                     10043.298 Million cell updates/sec

Title:          US-10-054-536-2
Perfect score:  747
Sequence:       1 atgtccctgttccatcact.........tctgtgagttccctactga 747

Scoring table:  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:   4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters:       9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      GenEmbl:*
                1: gb_ba:*
                2: gb_htg:*
                3: gb_in:*
                4: gb_om:*
                5: gb_ov:*
                6: gb_pat:*
                7: gb_ph:*
                8: gb_pl:*
                9: gb_pr:*
               10: gb_ro:*
               11: gb_sts:*
               12: gb_sy:*
               13: gb_un:*
               14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                      SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	747	100.0	747	6	E27637	E27637 Recombinant
2	747	100.0	900	6	AR182149	AR182149 Sequence
3	747	100.0	1632	6	CQ875887	CQ875887 Sequence
4	747	100.0	1632	9	HOSA16576	Y16576 Homo sapien
5	747	100.0	1638	6	CQ875888	CQ875888 Sequence
6	747	100.0	1638	6	CQ875891	CQ875891 Sequence
7	747	100.0	1638	6	CQ875893	CQ875893 Sequence
8	747	100.0	1638	9	HOSA16577	Y16577 Homo sapien
9	747	100.0	1638	9	HOSA16580	Y16580 Homo sapien
10	747	100.0	1638	9	HOSA16581	Y16581 Homo sapien
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12	747	100.0	3605	6	AX411061	AX411061 Sequence
13	747	100.0	3605	9	HSMBPC	X15422 Human mRNA
14	745.4	99.8	960	6	BC069338	BC069338 Homo sapi
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23	599	80.2	678	6	CQ722821	CQ722821 Sequence
24	587.8	78.7	805	9	D73408	D73408 Bos taurus
25	444.6	59.5	1409	4	AF164576	AF164576 Sus scrof
26	406.6	54.4	723	4	E37364	E37364 Swine serum
27	395	52.9	1010	6	MACMBPA	L43912 Macaca mula
28	381.4	51.1	799	9	MACMBPA	L43912 Macaca mula
29	374.8	50.2	1116	10	S42294	S42294 mannose-bin
30	374	50.1	1254	9	HSMBP1D	X15957 H.sapiens M
31	374	50.1	3336	9	HSMBPCA3	AF080510 Homo sapi
32	373.2	50.0	1069	10	MUSRRFA	D11440 Mus musculu
33	373.2	50.0	1098	10	BC010760	BC010760 Mus muscu
34	372.4	49.9	374	9	AY707499S4	AY707499 Gorilla g
35	372.4	49.9	102532	9	AL731550	AL731550 Human DNA	c
36	370.8	49.6	374	9	AY70748484	AY707487 Pan trogl
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38	366.2	49.0	874	10	RNMBPR	X05023 Rat mRNA fo
39	364.6	48.8	1037	6	AX402034	AX402034 Sequence
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42	353.2	47.3	374	9	AY70750484	AY707507 Hylobates
43	351.6	47.1	374	9	AY70750084	AY707503 Hylobates
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45	334	44.7	374	9	AY70747684	AY707479 Papio pap

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                            ALIGNMENTS

RESULT 1
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LOCUS       E27637              747 bp    DNA        linear    PAT 18-JUN-2001
DEFINITION  Recombinant human mannan binding protein and process for producing
            the same.
ACCESSION   E27637
VERSION     E27637.1  GI:13018239
KEYWORDS    JP 199206378-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   Nobutaka,W.
  TITLE     Recombinant human mannan binding protein and process for producing
            the same
  JOURNAL   Patent: JP 199206378-A 2 03-AUG-1999;
            FUSO YAKUHIN KOGYO KK
  OS        Unidentified
  PN        JP 199206378-A/2
  PD        03-AUG-1999
  PF        23-JAN-1998 JP 1998011864
  PI        NOBUTAKA WAKAMIYA
  PC        C12N15/09,C07K14/47,C12P21/02//A61K38/00,(C12N15/09,C12R1:91),
  PC        (C12P21/02,C12R1:91),C12N15/00,A61K37/02,(C12N15/00,C12R1:91)
  CC        Strandedness: Double;
  CC        Topology: Linear;
  FH        Key             Location/Qualifiers
  FT        source          1..747
  FT                        /organism='Unidentified'.

FEATURES             Location/Qualifiers
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ORIGIN
Query Match             100.0%;  Score 747;  DB 6;  Length 747;
Best Local Similarity   100.0%;  Pred. No. 7.5e-209;
Matches  747;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 ATGTCCCTGTTCCATCACTCCCTCCCTCCTCCTCCTCCTGAGTATGGTGGCAGCGTCTTACTCA  60
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Best Local Similarity   100.0%;  Pred. No. 7.7e-209;
Matches 747;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy    61 GAAACTGTGACCTGTGAGGATGGCGTCCTGACGATTGCCTGTGAGCTCT 120
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Qy   121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
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Db   186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy   181 GAACCAGGCCAAGGGCTTCAGAGGCTTACAGGGCCTTGGGGGCCTTCCAGGA 240
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Qy   241 AATCCAGGGCCTTCTGGGTCACCAGGACCCAAAGGGCCAAAAGGGCCAAAAGT 300
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Db   306 AATCCAGGGCCTTCTGGGTCACCAGGACCCAAAGGGCCAAAAGGGCCAAAAGT 365

Qy   301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAGCTCTGCAAACAGAAATGGCA 360
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Db   366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAGCTCTGCAAACAGAAATGGCA 425

Qy   361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
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Db   426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy   421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTGTCAAGTTCCAGGCC 480
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Qy   481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
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Db   546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy   541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
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Qy   601 AATAGACTGACCTACACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
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Qy   661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
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Db   726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy   721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
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Db   786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812
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RESULT 3
CQ875887
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LOCUS       CQ875887                1632 bp    DNA        linear      PAT 04-OCT-2004
DEFINITION  Sequence 20 from Patent WO2004065626.
ACCESSION   CQ875887
VERSION     CQ875887.1  GI:53789630
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Garred,P., Madsen,H.O. and str M.J.
TITLE       A method of sepsis prognosis
JOURNAL     Patent: WO 2004065626-A 20 05-AUG-2004;
            Rigshospitalet (DK); Kobenhavns Amt (DK)
FEATURES    Location/Qualifiers
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Db            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1 ATGTCCCTGTTCCATCACTCCCTCCTTCCTTCCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60

Qy    61 GAAACTGTGACCTGTGAGGATGGCGTCCTGACGATTGCCTGTGAGCTCT 120
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Db    61 GAAACTGTGACCTGTGAGGATGGCGTCCTGACGATTGCCTGTGAGCTCT 120

Qy   121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
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Qy   181 GAACCAGGCCAAGGGCTTCAGAGGCTTACAGGGCCTTGGGGGCCTTCCAGGA 240
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Qy   241 AATCCAGGGCCTTCTGGGTCACCAGGACCCAAAGGGCCAAAAGGGCCAAAAGT 300
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Qy   301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAGCTCTGCAAACAGAAATGGCA 360
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Qy   361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
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Db   361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420

Qy   421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTGTCAAGTTCCAGGCC 480
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Db   421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTGTCAAGTTCCAGGCC 480

Qy   481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
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Db   481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540

Qy   541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
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Db   541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600

Qy   601 AATAGACTGACCTACACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
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Db   601 AATAGACTGACCTACACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660

Qy   661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
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Db   661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720

Qy   721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
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RESULT 2
AR182149
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LOCUS       AR182149                 900 bp    DNA        linear      PAT 20-APR-2002
DEFINITION  Sequence 1 from patent US 6337193.
ACCESSION   AR182149
VERSION     AR182149.1  GI:20225065
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 900)
AUTHORS     Tully,R.E., Caltagirone,G.Thomas., Moyer,S.S. and Ronning,M.T.
TITLE       Expression of manose-binding protein in methylotrophic yeast
JOURNAL     Patent: US 6337193-A 1 08-JAN-2002;
FEATURES    Location/Qualifiers
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Best Local Similarity 100.0%;   Pred. No. 8.2e-209;
Matches  747;   Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy   61 GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT   120
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Qy  121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG  180
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Qy  181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCTGGAAAGTTGGGGCCTCCAGGA   240
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Qy  241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGGCAAAAGGGAGACCCTGGAAAAAGT  300
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Qy  301 CCGGATGGTGATAGTAGCCTGCTCAGAAAGAAAAGTCTGCAAACAGAAATGGCA  360
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Db 1186 CCGGATGGTGATAGTAGCCTGCTGCCTGCTCAGAAAGAAAAGTCTGCAAACAGAAATGGCA  1245

Qy  361 CGTATCAAAAAGTGGCTGACCTTCTCTCGGGCAAACAAGTTGGGAACAAGTTCTTCCTG  420
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Qy  421 ACCAATGGTGAAATAATGACCTTTGAAAAGTGAAGGCCTTGTGTGTCAGTTCCAGGCC  480
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Qy  481 TCTGTGGCCACCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG  540
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Qy  541 GAAGCCTTCCTGGCCATCACTGATGAGAAGACAGAAGGGCAGTTTGTTGGATCTGACAGGA  600
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Qy  661 GATTGTGTATTGCTACTGAAAAAATGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT  720
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Qy  721 CTTGGGCCGTCTGTGAGTTCCTATCTGA   747
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Db 1606 CTGGGCCCTCGTGAGTTCCCTATCTGA  1632
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RESULT 4
LOCUS   HOSA16576   1632 bp   DNA   linear   PRI 17-SEP-1999
DEFINITION Homo sapiens gene encoding mannan/mannose-binding protein, variant
            LYQA.
ACCESSION   Y16576
VERSION   Y16576.1 GI:5911789
KEYWORDS   mannose-binding lectin; mbl gene.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Madsen,H.O., Satz,M.L., Hogh,B., Svejgaard,A. and Garred,P.
  TITLE   Different molecular events result in low protein levels of
            mannan-binding lectin in populations from southeast Africa and
            South America
  JOURNAL   J. Immunol. 161 (6), 3169-3175 (1998)
  MEDLINE   98414317
  PUBMED   9743385
REFERENCE   2 (bases 1 to 1632)
  AUTHORS   Madsen,H.O.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-FEB-1998) H.O. Madsen, Department of Clinical
            Immunology, Section 7631, National University Hospital, Tagensvej
            20, DK-2200 Copenhagen, DENMARK
COMMENT   Related sequences X15954, X15955, X15956, X15422.
FEATURES   Location/Qualifiers
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Qy  181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCCTGGAAAGTTGGGGCCTCCAGGA  240
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RESULT 5
CQ875888

LOCUS   CQ875888   1638 bp   DNA   linear   PAT 04-OCT-2004
DEFINITION Sequence 21 from Patent WO2004065626.
ACCESSION   CQ875888
VERSION   CQ875888.1   GI:53789631
KEYWORDS
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Garred,P., Madsen,H.O. and str M,J.

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Best Local Similarity  100.0%;  Pred. No. 8.2e-209;
Matches 747;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy  421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCAGGAG  480
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RESULT 6
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LOCUS   CQ875891   1638 bp   DNA   linear   PAT 04-OCT-2004
DEFINITION Sequence 24 from Patent WO2004065626.
ACCESSION   CQ875891
VERSION   CQ875891.1   GI:53789634

KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
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              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS   Garred,P., Madsen,H.O. and str M,J.
TITLE   A method of sepsis prognosis
JOURNAL   Patent: WO 200406526-A 24 05-AUG-2004;
              Rigshospitalet (DK); Kobenhavns Amt (DK)
FEATURES   Location/Qualifiers
source   1..1638
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Query Match   100.0%;   Score 747; DB 6; Length 1638;
Best Local Similarity 100.0%;   Pred. No. 8.2e-209;
Matches 747; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   1612 CTGCGCCGTCTGTGAGTTCCCTATCTGA 1638
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LOCUS       HOSA16577              1638 bp    DNA     linear   PRI 17-SEP-1999
DEFINITION  Homo sapiens gene encoding mannan/mannose-binding protein, variant
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ACCESSION   Y16577
VERSION     Y16577.1  GI:5911791
KEYWORDS    mannose-binding lectin; mbl gene.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Madsen,H.O., Satz,M.L., Hogh,B., Svejgaard,A. and Garred,P.
TITLE       Different molecular events result in low protein levels of
            mannan-binding lectin in populations from southeast Africa and
            South America
JOURNAL     J. Immunol. 161 (6), 3169-3175 (1998)
MEDLINE     98414317
PUBMED      9743385
REFERENCE   2  (bases 1 to 1638)
AUTHORS     Madsen,H.O.
TITLE       Direct Submission
JOURNAL     Submitted (16-FEB-1998) H.O. Madsen, Department of Clinical
            Immunology, Section 7631, National University Hospital, Tagensvej
            20, DK-2200 Copenhagen, DENMARK
COMMENT     Related sequences X15954, X15955, X15956, X15422.
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Best Local Similarity   100.0%;  Pred. No. 8.2e-209;
Matches  747;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
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Qy   241 AATCCAGGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAGGAGACACCCTGGAAAAAGT 300
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Qy    721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
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Db   1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638
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RESULT 9
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LOCUS   HOSA16580   1638 bp   DNA   linear   PRI 17-SEP-1999
DEFINITION Homo sapiens gene encoding mannan/mannose-binding protein, variant
            LXPA.
ACCESSION   Y16580
VERSION   Y16580.1 GI:5911797
KEYWORDS   mannose-binding lectin; mbl gene.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS   Madsen,H.O., Satz,M.L., Hogh,B., Svejgaard,A. and Garred,P.
TITLE   Different molecular events result in low protein levels of
            mannan-binding lectin in populations from southeast Africa and
            South America
JOURNAL   J. Immunol. 161 (6), 3169-3175 (1998)
MEDLINE   98414317
PUBMED   9743385
REFERENCE   2 (bases 1 to 1638)
AUTHORS   Madsen,H.O.
TITLE   Direct Submission
JOURNAL   Submitted (16-FEB-1998) H.O. Madsen, Department of Clinical
            Immunology, Section 7631, National University Hospital, Tagensvej
            20, DK-2200 Copenhagen, DENMARK
COMMENT   Related sequences X15954, X15955, X15956, X15422.
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Query Match   100.0%;   Score 747; DB 9; Length 1638;
Best Local Similarity   100.0%;   Pred. No. 8.2e-209;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 ATGTCCCTGTTTCCATCACTCCCTCTCCTCCTCTCTCCTGAGTATGGTGGCAGCGTCTACTCA 60
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Db    892 ATGTCCCTGTTTCCATCACTCCCTCTCCTCCTCTCTCCTGAGTATGGTGGCAGCGTCTACTCA 951

Qy     61 GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCAGTGATTGCCTGAGCTCT 120
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Db    952 GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCAGTGATTGCCTGAGCTCT 1011

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Qy    181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCTGGGAAGTTGGGGCCTCCAGGA 240
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Db   1192 CCGGATGGTGATAGTAGCCTGGCTGGCTGCCTCAGAAGAAAGCTCGCAAACAGAAATGGCA 1251

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Db   1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy    481 TCTGTGGCCACCCCAGGAATGGCTGCAGAGATGTGCAGAGAATGGAGCCATTCATCAAGGAG 540
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Db   1372 TCTGTGGCCACCCCAGGAATGGCTGCAGAGATGTGCAGAGAATGGAGCCATTCATCAAGGAG 1431

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Db   1432 GAAGCCTTCCTGGCATCACTGATGAGAAGACAGGGCAGTTGTGATCTGACAGGA 1491

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Db   1492 AATAGACTGACCTACACAAACTGGAACGAGGGGTGAACCCAACAATGCTGGTTCTGATGAA 1551

Qy    661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
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Db   1612  CTGGCCGTCTGTGAGTTCCCTATCTGA 1638
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RESULT 10
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LOCUS   HOSA16581   1638 bp   DNA   linear   PRI 17-SEP-1999
DEFINITION Homo sapiens gene encoding mannan/mannose-binding protein, variant
            HYPA.
ACCESSION   Y16581
VERSION   Y16581.1 GI:5911806
KEYWORDS   mannose-binding lectin; mbl gene.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS   Madsen,H.O., Satz,M.L., Hogh,B., Svejgaard,A. and Garred,P.
TITLE   Different molecular events result in low protein levels of
            mannan-binding lectin in populations from southeast Africa and
            South America
JOURNAL   J. Immunol. 161 (6), 3169-3175 (1998)
MEDLINE   98414317
PUBMED   9743385
REFERENCE   2 (bases 1 to 1638)
AUTHORS   Madsen,H.O.
TITLE   Direct Submission
JOURNAL   Submitted (16-FEB-1998) H.O. Madsen, Department of Clinical
            Immunology, Section 7631, National University Hospital, Tagensvej
            20, DK-2200 Copenhagen, DENMARK
COMMENT   Related sequences X15954, X15955, X15956, X15422.
FEATURES   Location/Qualifiers
     source   1..1638
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                     /chromosome="10"
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                     /note="MBL haplotype HYPA"
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     variation   826
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     variation   1061
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Query Match   100.0%; Score 747; DB 9; Length 1638;
Best Local Similarity 100.0%; Pred. No. 8.2e-209;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGTCCCTGTTTCCATCACTCCCTCCTTCCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
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Db   892 ATGTCCCTGTTTCCATCACTCCCTCCTTCCTCCTGAGTATGGTGGCAGCGTCTTACTCA 951

Qy   61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCCGTGATTGCCTGTAGCTCT 120
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Qy   181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
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Db 1072 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy   241 AATCCAGGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAGGAGACCCTGGAAAAAGT 300
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Db 1132 AATCCAGGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAGGAGACCCTGGAAAAAGT 1191

Qy   301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAGAAAGCTCTGCAAACAGAAATGGCA 360
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Db 1192 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAGAAAGCTCTGCAAACAGAAATGGCA 1251

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Db 1252 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAACAAGTTGGAACAAGTTCTTCCTG 1311

Qy   421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
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Db 1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy   481 TCTGTGGCCACCCCCAGGAATGCTGCGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
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Db 1372 TCTGTGGCCACCCCCAGGAATGCTGCGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy   541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
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Qy   661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
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Qy   721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
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RESULT 11

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E27636
LOCUS       E27636              3605 bp    DNA    linear    PAT 18-JUN-2001
DEFINITION  Recombinant human mannan binding protein and process for producing
            the same.
ACCESSION   E27636
VERSION     E27636.1  GI:13018238
KEYWORDS    JP 1999206378-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3605)
  AUTHORS   Nobutaka,W.
  TITLE     Recombinant human mannan binding protein and process for producing
            the same
  JOURNAL   Patent: JP 1999206378-A 1 03-AUG-1999;
            FUSO YAKUHIN KOGYO KK
COMMENT     OS   Homo sapiens
            PN   JP 1999206378-A/1
            PD   03-AUG-1999
            PF   23-JAN-1998 JP 1998011864
            PR
            PI   NOBUTAKA WAKAMIYA
            PC   C12N15/09,C07K14/47,C12P21/02//A61K38/00, (C12N15/09,C12R1:91),
            PC   (C12P21/02,C12R1:91),C12N15/00,A61K37/02, (C12N15/00,C12R1:91)
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   sig peptide     66..125
            FT   CDS             66..812.
FEATURES             Location/Qualifiers
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Query Match            100.0%;  Score 747;  DB 6;  Length 3605;
Best Local Similarity  100.0%;  Pred. No. 9.1e-209;
Matches  747;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1  ATGTCCCTGTTTCCATCACTCCCTCTCCTTCCTGAGTATGGTGGCAGCGTCTTACTCA  60
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Db    66  ATGTCCCTGTTTCCATCACTCCCTCTCCTTCCTGAGTATGGTGGCAGCGTCTTACTCA  125

Qy    61  GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126  GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT  185

Qy   121  CCAGGCATCAACGGCTTCCCAGGCCAAGATGGCGTGATGGCACCAAGGGAGAAAAGGGG  180
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Db   186  CCAGGCATCAACGGCTTCCCAGGCCAAGATGGCGTGATGGCACCAAGGGAGAAAAGGGG  245

Qy   181  GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTGGGGCCTCCAGGA  240
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Db   246  GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTGGGGCCTCCAGGA  305

Qy   241  AATCCAGGGCCCTTGATAGTAGTGGCTGAGAAGAAAAGCTCTGCAAACAGAAATGGCA  360
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Db   306  CCGGATGGTGATAGTAGTGGCTGAGAAGAAAAGCTCTGCAAACAGAAATGGCA  425
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RESULT 12

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AX411061
LOCUS       AX411061            3605 bp    DNA    linear    PAT 14-JUN-2002
DEFINITION  Sequence 3708 from Patent WO0229103.
ACCESSION   AX411061
VERSION     AX411061.1  GI:21443766
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
  TITLE     Gene expression profiles in liver cancer
  JOURNAL   Patent: WO 0229103-A 3708 11-APR-2002;
            GENE LOGIC INC (US)
FEATURES             Location/Qualifiers
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ORIGIN

Query Match            100.0%;  Score 747;  DB 6;  Length 3605;
Best Local Similarity  100.0%;  Pred. No. 9.1e-209;
Matches  747;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1  ATGTCCCTGTTTCCATCACTCCCTCTCCTTCCTGAGTATGGTGGCAGCGTCTTACTCA  60
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Qy    61  GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT  120
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Db   126  GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT  185

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Db   186  CCAGGCATCAACGGCTTCCCAGGCCAAGATGGCGTGATGGCACCAAGGGAGAAAAGGGG  245

Qy   181  GAACCAGGCCAAGGGCTTACAGGGCTTACAGGGCCCAAGGGCCAAAGGGCCTCCAGGA  240
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Db   246  GAACCAGGCCAAGGGCTTACAGGGCTTACAGGGCCCAAGGGCCAAAGGGCCTCCAGGA  305

Qy   241  AATCCAGGGCCCTTCGGGTCACCAGGACCAAAAGGGCCAAAAGGGCCTCGAAAAAGT  300
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Db   306  AATCCAGGGCCCTTCGGGTCACCAGGACCAAAAGGGCCAAAAGGGCCTCGAAAAAGT  365

Qy   421  ACCAATGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC  480
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Db   486  ACCAATGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC  545

Qy   481  TCTGTGGCCACCCCAGGAATGCTGCGAGAATGTGCGAGAATCTCATCAAGAG  540
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Db   546  TCTGTGGCCACCCCAGGAATGCTGCGAGAATGTGCGAGAATCTCATCAAGAG  605

Qy   541  GAAGCCTTCCTGGCCATCACTGATGAGAAGACAGAGGGCAGTTGTGGATCTGACAGA  600
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Db   606  GAAGCCTTCCTGGCCATCACTGATGAGAAGACAGAGGGCAGTTGTGGATCTGACAGA  665

Qy   601  AATAGACTGACCTACACAAACTGGAACGAGAGGGTGAACCAACAATGCTGGTTCTGATGAA  660
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Qy   721  CTGGCCGTCTGTGAGTTCCCTATCTGA  747
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sig_peptide     66..125
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mat_peptide     126..809
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ORIGIN

Query Match           100.0%;   Score 747;   DB 9;   Length 3605;
Best Local Similarity 100.0%;   Pred. No. 9.1e-209;
Matches  747;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1  ATGTCCCTGTTCCATCACTCCCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA  60
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Db    66  ATGTCCCGTTTCCATCACTCCCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA  125

Qy    61  GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT  120
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Db   126  GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT  185

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Db   186  CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGGTGATGGCACCAAGGGAGAAAAGGGG  245

Qy   181  GAACCAGGCCAAGGGCTTCACGGGGCCCCCCGAAAGTTGGGGCCCTCCAGGA  240
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Db   246  GAACCAGGCCAAGGGCTCAGAGGGCTTCACGGGGCCCCCCGAAAGTTGGGGCCCTCCAGGA  305

Qy   241  AATCCAGGGCCTTCCTGGGTCACCAGGACCAAAGGGCCAAAAGGAGACCCTGGAAAAGT  300
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Db   306  AATCCAGGGCCTTCCTGGGTCACCAGGACCAAAGGGCCAAAAGGAGACCCTGGAAAAGT  365

Qy   301  CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAGAAAGCTCTGCAAACAGAAATGGCA  360
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Db   366  CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAGAAAGCTCTGCAAACAGAAATGGCA  425

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Qy   541  GAAGCCTTCCTGGGCATCACACAAACTGAACAGACTGAACCCAACAATGCTGGTTCTGATGAA  600
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Qy   601  AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA  660
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Qy   661  GATTGTGTATTGCTACTGAAAAAATGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT  720
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Qy   301  CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAGAAAGCTCTGCAAACAGAAATGGCA  360
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DEFINITION  Human mRNA for mannose-binding protein C.
ACCESSION   X15422
VERSION     X15422.1  GI:34486
KEYWORDS    mannose-binding protein.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3605)
  AUTHORS   Sastry,K., Herman,G.A., Day,L., Deignan,E., Bruns,G., Morton,C.C.
            and Ezekowitz,R.A.
  TITLE     The human mannose-binding protein gene. Exon structure reveals its
            evolutionary relationship to a human pulmonary surfactant gene and
            localization to chromosome 10
  JOURNAL   J. Exp. Med. 170 (4), 1175-1189 (1989)
  MEDLINE   90010778
   PUBMED   2477486
REFERENCE   2  (bases 1 to 3605)
  AUTHORS   Ezekowitz,R.A.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-1989) Ezekowitz R.A.B., The Children's Hospital,
            Enders Building 7th Floor, 300 Longwood Avenue, Boston MA 02115, U
            S A
COMMENT     X15422 revises MBP cDNA seq published by:
            Ezekowitz et. al. J. Exp. Med. 167:1034-1046(1988). Data kindly
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DEFINITION  Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic
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ACCESSION   BC069338
VERSION     BC069338.1  GI:46854807
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 960)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
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            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED    12477932
REFERENCE   2  (bases 1 to 960)
  AUTHORS   .
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Baylor Human Genome Sequencing Center
            cDNA Library Preparation: Baylor Human Genome Sequencing Center
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.
            Clone distribution: MGC clone distribution information can be found
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Search completed: June 20, 2005, 17:02:04
Job time : 3608 secs

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VERSION   CQ875889.1 GI:53789632
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REFERENCE   1
  AUTHORS   Garred,P., Madsen,H.O. and str M,J.
  TITLE   A method of sepsis prognosis
  JOURNAL   Patent: WO 200405626-A 22 05-AUG-2004;
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ORIGIN

Query Match   99.8%;   Score 745.4; DB 6; Length 1632;
Best Local Similarity   99.9%; Pred. No. 2.4e-208;
Matches 746; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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.OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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            Pred. No. is the number of results predicted by chance to have a
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25	635.8	85.1	963	1	AAN91079		Aan91079 cDNA of h
26	444.6	59.5	1409	6	AAD45344		Aad45344 Human ant
27	395	52.9	1010	9	AAA70738		Aaa70738 Pig serum
28	364.6	50.1	3336	2	AAQ64652		Aaq64652 Human Man
29	364.6	48.8	1037	6	ABK63803		Abk63803 Rat seque
30	364.6	48.8	1037	10	ADB58487		Adb58487 Toxicity-
31	287.6	38.5	1068	12	ADP71919		Adp71919 Renal tox
32	286	38.3	717	10	ADB58066		Adb58066 Toxicity-
33	286	38.3	717	10	ADB52544		Adb52544 Primary r
34	284.4	38.1	943	4	AAH44805		Aah44805 Murine cD
35	280.6	37.6	1437	4	AAK51894		Aak51894 Human pol
36 c	274.4	36.7	1662	4	AAK52878		Aak52878 Human pol
37	240.6	32.2	1248	12	ADP28880		Adp28880 Human sec
38 c	224	30.0	1143	12	ADO21125		Ado21125 Human car
39	222	29.7	419	8	ABX46620		Abx46620 Bovine ES
40	204.4	27.4	1211	6	ABK14789		Abk14789 DNA encod
41	188	25.2	1802	2	AAQ53530		Aaq53530 Human Man
42	186.2	24.9	405	6	ABS66633		Abs66633 Rat PrMBP
43	186	24.9	1802	10	ABX08715		Abx08715 Pathogeni
44	186	24.9	1802	10	ABX08719		Abx08719 Pathogeni
45	186	24.9	1802	10	ABX08711		Abx08711 Pathogeni

```
                              ALIGNMENTS

RESULT 1
AAZ07142
ID   AAZ07142 standard; cDNA; 747 BP.
XX
AC   AAZ07142;
XX
DT   11-OCT-1999  (first entry)
XX
DE   Human mannan-binding protein encoding cDNA.
XX
KW   Human; mannan-binding protein; hMBP; recombinant; inhibition; infection;
KW   rhMBP; haemagglutination; influenza; HIV; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9937676-A1.
XX
PD   29-JUL-1999.
XX
PF   23-JUL-1998;   98WO-JP003311.
XX
PR   23-JAN-1998;   98JP-00011864.
XX
PA   (FUSO ) FUSO PHARM IND LTD.
XX
PI   Wakamiya N;
XX
DR   WPI; 1999-469114/39.
DR   P-PSDB; AAY29485.
XX
PT   Recombinant human mannan-binding protein expressed using pNOW1 vector.
XX
PS   Example 2; Page 74; 91pp; Japanese.
XX
CC   The present invention describes recombinant human mannan-binding protein
CC   (rhMBP) having a molecular weight range of 1000-1300 or 200-400 kDa (by
CC   gel filtration with detection at 280 nm). rhMBP may be used as a
CC   component of drug compositions for the inhibition of haemagglutination
CC   and prevention of infection by viruses such as influenza and HIV. The
CC   present sequence encodes hMBP (human mannan-binding protein).
XX
SQ   Sequence 747 BP; 203 A; 187 C; 202 G; 155 T; 0 U; 0 Other;
```

Query Match　　100.0%;　Score 747;　DB 2;　Length 747;
Best Local Similarity　100.0%;　Pred. No. 1.1e-207;
Matches 747;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

```
Qy    1  ATGTCCCGTTCCATCACTCCCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA   60
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Db    1  ATGTCCCGTTCCATCACTCCCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA   60

Qy   61  GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGATTGCCTGTAGCTCT  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGATTGCCTGTAGCTCT  120

Qy  121  CCAGGCATCAACGGCTTCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAGGGG  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  CCAGGCATCAACGGCTTCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAGGGG  180

Qy  181  GAACCAGGCCAAGGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  GAACCAGGCCAAGGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA  240

Qy  241  AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT  300

Qy  301  CCGGATGGTGATAGTAGCCAGTTTGTGATCTGACAGGA  360
         ||||||||||||||||||||||||||||||||||||||
Db  301  CCGGATGGTGATAGTAGCCAGTTTGTGATCTGACAGGA  360

Qy  361  CGTATCAAAAAGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTCAAGTTCCAGGCC  420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  CGTATCAAAAAGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTCAAGTTCCAGGCC  420

Qy  421  ACCAATGGTGATAGGCCTTGTGTCTTGTGTGTCAGTTCAAGTCTCATCAAGGAG  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  ACCAATGGTGATAGGCCTTGTGTCTTGTGTGTCAGTTCAAGTCTCATCAAGGAG  480

Qy  481  TCTGTGGCCACCCCAGGAATGCCAGTTGAGCCATTCAGAATCTCATCAAGGAG  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  TCTGTGGCCACCCCAGGAATGCCAGTTGAGCCATTCAGAATCTCATCAAGGAG  540

Qy  541  GAAGCCTTCCTGGCATCACTGATGAGAAGACAGAGGGCAGTTTGTGGATCTGACAGGA  600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  GAAGCCTTCCTGGCATCACTGATGAGAAGACAGAGGGCAGTTTGTGGATCTGACAGGA  600

Qy  601  AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGGCTGAATGAA  660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGGCTGAATGAA  660

Qy  661  GATTGTGTATTGCTACTGAAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  GATTGTGTATTGCTACTGAAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT  720

Qy  721  CTGGCCCGTCTGTGAGTTCCCTATCTGA  747
         ||||||||||||||||||||||||||||
Db  721  CTGGCCCGTCTGTGAGTTCCCTATCTGA  747
```

RESULT 2
ADI20100
ID　ADI20100 standard; DNA; 747 BP.
XX
AC　ADI20100;
XX
DT　22-APR-2004 (first entry)
XX
DE　DNA sequence #2 related to the invention.
XX
KW　anti-human immunodeficiency virus; HIV; mannose binding protein; MBP; ds.
XX
OS　Homo sapiens.
XX
PN　WO2004002511-A1.
XX

PD　08-JAN-2004.
XX
PF　30-JUN-2003; 2003WO-JP008259.
XX
PR
PA　28-JUN-2002; 2002JP-00189534.
XX
PA　(FUSO) FUSO PHARM IND LTD.
XX
PI　Wakamiya N, Ohtani K, Sakamoto T, Keshi H, Kishi Y;
XX
DR　WPI; 2004-082879/08.
XX
PT　Anti-human immunodeficiency virus (HIV) agent comprising a mannose
PT　binding protein for treatment of HIV infection.
XX
PS　Disclosure; SEQ ID NO 2; 44pp; Japanese.
XX
CC
CC　The present invention relates to anti-human immunodeficiency virus (HIV)
CC　agent comprises a mannose binding protein (MBP). For use in the treatment
CC　of HIV. The present sequence represents a DNA sequence related to the
CC　invention.
XX
SQ　Sequence 747 BP; 203 A; 187 C; 202 G; 155 T; 0 U; 0 Other;

Query Match　100.0%;　Score 747;　DB 12;　Length 747;
Best Local Similarity　100.0%;　Pred. No. 1.1e-207;
Matches 747;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

```
Qy    1  ATGTCCCGTTCCATCACTCCCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA   60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  ATGTCCCGTTCCATCACTCCCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA   60

Qy   61  GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGATTGCCTGTAGCTCT  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGATTGCCTGTAGCTCT  120

Qy  121  CCAGGCATCAACGGCTCCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAGGGG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  CCAGGCATCAACGGCTCCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAGGGG  180

Qy  181  GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCTGGAAAGTTGGGGCCTCCAGGA  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCTGGAAAGTTGGGGCCTCCAGGA  240

Qy  241  AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT  300

Qy  301  CCGGATGGTGATAGTAGCCAGTTTGTGATCTGACAGGA  360
         ||||||||||||||||||||||||||||||||||||||
Db  301  CCGGATGGTGATAGTAGCCAGTTTGTGATCTGACAGGA  360

Qy  361  CGTATCAAAAAGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTCAAGTTCCAGGCC  420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  CGTATCAAAAAGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTCAAGTTCCAGGCC  420

Qy  421  ACCAATGGTGATAGCCAACAAAGTCGGAACGAGGCCTTGTGTCAGTTCAAGTTCATCAAGGAG  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  ACCAATGGTGATAGCCAACAAAGTCGGAACGAGGCCTTGTGTCAGTTCAAGTTCATCAAGGAG  540

Qy  541  TCTGTGGCCACCCCAGGAATGCTGCAGTTGAGCCATTCAGAATCTCATCAAGGAG  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  TCTGTGGCCACCCCAGGAATGCTGCAGTTGAGCCATTCAGAATCTCATCAAGGAG  540

Qy  541  GAAGCCTTCCTGGCATCACTGATGAGAAGACAGAGGGCAGTTTGTGGATCTGACAGGA  600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  GAAGCCTTCCTGGCATCACTGATGAGAAGACAGAGGGCAGTTTGTGGATCTGACAGGA  600

Qy  601  AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGGCTGAATGAA  660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGGCTGAATGAA  660

Qy  661  GATTGTGTATTGCTACTGAAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT  720
```

```
Db  661 GATTGTGTATTGCTACTACTGAGAAAAATGGCCAGTGGAATGGCAGTGGAATGACGTCCCCTGCTCCCACCTCCCAT 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
            |||||||||||||||||||||||||||
Db  721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
```

RESULT 3
ABK14771
ID   ABK14771 standard; DNA; 900 BP.
XX
AC   ABK14771;
XX
DT   08-MAY-2002 (first entry)
XX
DE   DNA encoding human mannose-binding protein (MBP).
XX
KW   Human; mannose-binding protein; MBP; methylotropic yeast strain;
KW   protein disulphide isomerase; PDI; heat shock protein 47; hsp47;
KW   propyl-4-hydroxylase; P4H; pathogenic organism disposal; biocide; gene;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   66..812
FT   /*tag= a
FT   /product= "Mannose-binding protein (MBP)"
XX
PN   US6337193-B1.
XX
PD   08-JAN-2002.
XX
PF   24-NOV-1998; 98US-00198603.
XX
PR   24-NOV-1998; 98US-00198603.
XX
PA   (APTA-) APTAGEN INC.
XX
PI   Tully RE, Caltagirone GT, Moyer SS, Ronning MT;
XX
DR   WPI; 2002-163238/21;
DR   P-PSDB; AAU75574;
XX
PT   Methylotrophic yeast strain, useful for producing mannose-binding
PT   protein, comprises DNA molecules encoding the protein, protein disulfide
PT   isomerase, heat shock protein 47 and propyl-4-hydroxylase.
XX
PS   Claim 5; Fig 1; 30pp; English.
XX
CC   The invention relates to a methylotrophic yeast strain (I) comprising a
CC   DNA molecule encoding mannose-binding protein (MBP), protein disulphide
CC   isomerase (PDI), heat shock protein 47 (hsp47), and propyl-4-hydroxylase
CC   (P4H), where upon culturing (I) produces the MBP, PDI, hsp47 and P4H. (I)
CC   is useful for producing MBP comprising culturing (I) under conditions
CC   suitable for the secretion of MBP by the yeast where MBP is utilised in
CC   disposal of pathogenic organisms by opsonising pathogen or activating
CC   complement cascade. The methods utilising (I) result in high yields of
CC   MBP without the use of foetal calf serum, in a cost-effective manner. The
CC   present sequence relates to the coding sequence of human mannose-binding
CC   protein
XX
SQ   Sequence 900 BP; 246 A; 225 C; 228 G; 201 T; 0 U; 0 Other;
```

```
Query Match            100.0%;  Score 747; DB 6; Length 900;
Best Local Similarity  100.0%;  Pred. No. 1.2e-207;
Matches 747;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1 ATGTCCCTGTTTCCATCACTCCCTCTTCCTCCTCCTGAGTATCGTGGCAGCGTCTTACTCA 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  66 ATGTCCCTGTTTCCATCACTCCCTCTTCCTCCTCCTGAGTATCGTGGCAGCGTCTTACTCA 125
```

```
Qy   61 GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCCCAGTGATGCCGTGAGCTCT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  126 GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCCCAGTGATGCCGTGAGCTCT 185

Qy  121 CCAGGCATCAACGGCTTCCCAGGCAAGATGGCGTGATGGCCACCAGGAGAAAAGGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  186 CCAGGCATCAACGGCTTCCCAGGCAAGATGGCGTGATGGCCACCAGGAGAAAAGGGG 245

Qy  181 GAACCAGGCCAAGGGCTTACAGGGCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  246 GAACCAGGCCAAGGGCTTACAGGGCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy  241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365

Qy  301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAGAAAAGCTCGCAAACAGAAATGGCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAGAAAAGCTCGCAAACAGAAATGGCA 425

Qy  361 CGTATCAAAAAGTGGCTGACCTTCTCTCGGCAAACAAGTGGGAACAAGTTCTTCCTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  426 CGTATCAAAAAGTGGCTGACCTTCTCTCGGCAAACAAGTGGGAACAAGTTCTTCCTG 485

Qy  421 ACCAATGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  486 ACCAATGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy  481 TCTGTGGCCACCCCCAGGAATGCTGCGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  546 TCTGTGGCCACCCCCAGGAATGCTGCGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy  541 GAAGCCTTCCTGGCATCACTGATGAGAACAGAGAGAGGCAGTTGTGATCTGACAGGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  606 GAAGCCTTCCTGGCATCACTGATGAGAACAGAGAGAGGCAGTTGTGATCTGACAGGA 665

Qy  601 AATAGACTGACCTACACAAACTGGAACAATGCTGGTTCGTGGTTCTGATGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  666 AATAGACTGACCTACACAAACTGGAACAATGCTGGTTCGTGGTTCTGATGAA 725

Qy  661 GATTGTGTATTGCTACTACTGAGAAAAATGGCCAGTGGAATGGCAGTGGAATGACGTCCCCTGCTCCCACCTCCCAT 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  726 GATTGTGTATTGCTACTACTGAGAAAAATGGCCAGTGGAATGGCAGTGGAATGACGTCCCCTGCTCCCACCTCCCAT 785

Qy  721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
          |||||||||||||||||||||||||||
Db  786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812
```

RESULT 4
ADR29055
ID   ADR29055 standard; DNA; 1632 BP.
XX
AC   ADR29055;
XX
DT   21-OCT-2004 (first entry)
XX
DE   Human MBL gene with non-structural/variant structural allele (codon 57).
XX
KW   Sepsis; septic shock; severe; MBL; mannose binding lectin; SIRS;
KW   systemic inflammatory response syndrome; innate immune defence;
KW   single nucleotide polymorphism; SNP; structural variant; regulatory;
KW   prophylaxis; sepsis syndrome; infection susceptibility;
KW   multiple organ failure; MOF; multiple organ dysfunction; acute; gene; ds;
KW   human.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   variation   396
FT   /*tag= a
FT   /standard_name= "Single nucleotide polymorphism"
FT   /note= "Non-structural allele"

```
FT   variation        474
FT                    /tag= b
FT                    /standard_name= "Single nucleotide polymorphism"
FT                    /note= "Non-structural allele"
FT   variation        487
FT                    /tag= c
FT                    /standard_name= "Single nucleotide polymorphism"
FT                    /note= "Non-structural allele"
FT   variation        747
FT                    /tag= d
FT                    /standard_name= "Single nucleotide polymorphism"
FT                    /note= "Non-structural allele"
FT   variation        820
FT                    /tag= e
FT                    /standard_name= "Single nucleotide polymorphism"
FT                    /note= "Non-structural allele"
FT   variation        1055
FT                    /tag= f
FT                    /standard_name= "Single nucleotide polymorphism"
FT                    /note= "Variant structural allele"
XX
PN   WO2004065626-A2.
XX
PD   05-AUG-2004.
XX
PF   16-JAN-2004; 2004WO-DK000027.
XX
PR   17-JAN-2003; 2003DK-00000042.
PR   06-MAR-2003; 2003US-0453272P.
XX
PA   (RIGS-) RIGSHOSPITALET.
PA   (KOBE-) KOBENHAVNS AMT.
XX
PI   Garred P, Madsen HO, Strom J;
XX
DR   WPI; 2004-571694/55.
XX
PT   Predicting whether an individual having Systemic Inflammatory Response
PT   Syndrome (SIRS) will develop sepsis, useful for treating sepsis,
PT   comprises determining the mannose-binding lectin (MBL) genotype or
PT   concentration of MBL.
XX
PS   Disclosure; SEQ ID NO 20; 65pp; English.
XX
CC   The invention relates to a method to determine the risk factor of a
CC   person for sepsis, severe sepsis or septic shock by correlating MBL
CC   (mannose binding lectin) genotype with a predefined risk value. It
CC   discloses the connection between the MBL genotype of an individual having
CC   SIRS (Systemic Inflammatory Response Syndrome) and the risk of developing
CC   sepsis, severe sepsis or septic shock. It shows how a decreased level of
CC   MBL and lack of functional MBL are crucial to the development of sepsis
CC   and septic shock in an individual having sepsis. A MBL is an important
CC   factor in innate immune defence. MBL single nucleotide polymorphism in
CC   the form of the structural variant (codon 54, codon 52 and codon 57) and
CC   regulatory variant (low expression and high expression) were studied.
CC   This invention discloses that the MBL gene polymorphism's causes a
CC   rapid determination of MBL genotype of patients is important in
CC   identifying individuals at risk of developing sepsis, severe sepsis or
CC   septic shock. The MBL can be used for a medicament for the prevention and
CC   reduction of the MBL level, which is associated with the development and
CC   progression of sepsis in adult intensive care patients. The invention
CC   offers a service to determine whether an individual belongs to a risk
CC   group and it provides the treatment accordingly. There is an increased
CC   risk of a fatal outcome of an individual carrying MBL variant alleles. A
CC   treatment of specified diseases. The MBL variant allele is also
CC   associated with an increased risk of death. It raises the prospective
CC   that MBL (MBL substitution) can be used in prophylaxis and treatment of
CC   sepsis syndrome. The frequency of MBL variant alleles is proportional to
CC   the severity of sepsis which indicates lacking buffering capacity of MBL
CC   towards initial microbial replication. It is not only associated with
CC   susceptibility of infection but also allows activation of host mechanisms
CC   central to the pathophysiology of the sepsis syndrome. The invention can
CC   also predict the risk for developing multiple organ failure (MOF),
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CC   multiple organ dysfunction and acute organ dysfunction of an individual
CC   having SIRS. The high risk is characterised by the presence of at least
CC   one variant structural allele of the MBL gene and or having two low
CC   expression regulatory alleles of the MBL gene in a sample. The presented
CC   sequence is the human MBL gene with non-structural and variant structural
CC   allele (codon 57).
XX
SQ   Sequence 1632 BP; 447 A; 381 C; 430 G; 374 T; 0 U; 0 Other;

Query Match         100.0%;  Score 747;  DB 13;  Length 1632;
Best Local Similarity 100.0%;  Pred. No. 1.6e-207;
Matches 747;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        1 ATGTCCCTGTTCCATCACTCCCTCTCCTTCCTTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      886 ATGTCCCTGTTCCATCACTCCCTCTCCTTCCTTCCTGAGTATGGTGGCAGCGTCTTACTCA 945

Qy       61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCTGCAGTTGATTGCCTGTAGCTCT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      946 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCTGCAGTTGATTGCCTGTAGCTCT 1005

Qy      121 CCAGGCATCAACGCTTCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1006 CCAGGCATCAACGGCTTCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 1065

Qy      181 GAACCAGGCCAAGGCTTACAGGGCCCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1066 GAACCAGGCCAAGGGCTTACAGGGCCCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1125

Qy      241 AATCCAGGGCCTTCTGGGTCACCAGGACCCAAAGGGACCAAAAGGAGACCCTGGAAAAAGT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1126 AATCCAGGGCCTTCTGGGTCACCAGGACCCAAAGGGACCAAAAGGAGACCCTGGAAAAAGT 1185

Qy      301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAGAAAGTCTGCAAACAGAAATGGCA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1186 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAGAAAGTCTGCAAACAGAAATGGCA 1245

Qy      361 CGTATCAAAAAGTGGCTGACCTTCTCTGGGCAAACAGTTCTTCTGGGCAAACAGTTCTTCCTG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1246 CGTATCAAAAAGTGGCTGACCTTCTCTGGGCAAACAGTTGGGCAAACAGTTCTTCCTG 1305

Qy      421 ACCAATGGTGAAATAATGACCTTTGAAAAGTGAAGGTGAAGGTGTGTGTCAAGTTCAAGTTCAGGCC 480
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Db     1306 ACCAATGGTGAAATAATGACCTTTGAAAAGTGAAGGTGAAGGTGTGTGTCAAGTTCAGGCC 1365

Qy      481 TCTGTGGCCACCCCACCGGAATGCTGCAGGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1366 TCTGTGGCCACCCCCACCGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1425

Qy      541 GAAGCCTTCCTGGCATCACTGATGAGAAGAACAGAGGGGACAGTTGTGGATCTGACAGGA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1426 GAAGCCTTCCTGGCATCACTGATGAGAAGAACAGAGGGGACAGTTGTGGATCTGACAGGA 1485

Qy      601 AATAGACTGACCTACACAAATGGAACGAGGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1486 AATAGACTGACCTACACAAACTGGAACGAGGGGTGAACCCAACAATGCTGGTTCTGATGAA 1545

Qy      661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCACCTCCCAT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1546 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCACCTCCCAT 1605

Qy      721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
            ||||||||||||||||||||||||||||
Db     1606 CTGGCCGTCTGTGAGTTCCCTATCTGA 1632
```

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RESULT 5
ADP03860
ID   ADP03860 standard; DNA; 1638 BP.
XX
AC   ADP03860;
XX
DT   29-JUL-2004 (first entry)
```

```
XX
DE   Human mbl2 DNA.
XX
KW   arteriosclerosis; severe heart disease; coronary heart disease; artery;
KW   polymorphism; human; mbl2; Chlamydia pneumoniae infection;
KW   mannose-binding lectin antigen; gene therapy; lectin-complement pathway;
KW   serine protease; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   variation      replace(273,g)
FT                  /*tag= a
FT   variation      replace(602,c)
FT                  /*tag= b
FT                  /standard_name= "single nucleotide polymorphism"
FT   CDS            821..1638
FT                  /*tag= c
FT                  /product= "MBL2"
FT   variation      replace(826,t)
FT                  /*tag= d
FT                  /standard_name= "single nucleotide polymorphism"
FT   variation      replace(1045,t)
FT                  /*tag= e
FT                  /standard_name= "single nucleotide polymorphism"
FT                  /note= "SNP reults in an Arg to Cys variation"
FT   variation      replace(1052,a)
FT                  /*tag= f
FT                  /standard_name= "single nucleotide polymorphism"
FT                  /note= "SNP results in a Gly to Asp variation"
FT   variation      replace(1061,a)
FT                  /*tag= g
FT                  /standard_name= "single nucleotide polymorphism"
FT                  /note= "SNP results in a Gly to Glu variation"
XX
PN   DE10237393-A1.
XX
PD   11-MAR-2004.
XX
PF   12-AUG-2002; 2002DE-01037393.
XX
PR   12-AUG-2002; 2002DE-01037393.
XX
PA   (LION-) LIONEX DIAGNOSTICS & THERAPEUTICS GMBH.
XX
PI   Fuerst G, Prohaszka Z, Gonczol E, Garred P, Madsen HO;
XX
DR   WPI; 2004-258256/25.
XX
PT   Determining risk of developing arteriosclerosis or coronary artery
PT   disease, by detecting both polymorphisms in the mbl2 gene and infection
PT   by Chlamydia pneumoniae.
XX
PS   Claim 2; Fig 1; 45pp; German.
XX
CC   This invention describes a novel method for determining an indicator of
CC   the risk of developing arteriosclerosis and severe heart disease of the
CC   coronary artery type by detecting polymorphisms in the human mbl2 gene
CC   and the presence of acute, chronic or early Chlamydia pneumoniae
CC   infection. The invention comprises detecting a low concentration of the
CC   MBL (= mannose-binding lectin) antigen instead of polymorphisms in mbl2,
CC   a diagnostic kit for performing the new tests, use of at least one
CC   specific polymorphism in mbl2 for determining the risk of
CC   arteriosclerosis or severe heart disease, use of recombinant or purified
CC   human MBL for treating patients, identified by the new method, who have
CC   mlb2 polymorphisms, use of polymorphic mbl2 genes for preparation of the
CC   polymorphic isoforms of MBL protein, and use of wild-type mbl2, or its
CC   fragments, for gene therapy of subjects who have mbl2 polymorphisms. The
CC   polymorphisms are stated as being at positions -551, -221 (the promoter
CC   region), +4 (untranslated region of exon 1), +52, +54, +57 or +223 (exon
CC   1), +230 and/or +239 of the sequence deposited as Genbank Y16580.
CC   Polymorphisms are detected in genomic DNA, especially isolated from
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CC   blood, by single-stranded conformational polymorphism, denaturing
CC   gradient gel electrophoresis, restriction fragment length polymorphism,
CC   sequencing or allele-specific dideoxy sequence termination and/or by
CC   ligase chain reaction. Alternatively, antibodies specific for polymorphic
CC   proteins are used. The MBL activity may be determined (in addition to, or
CC   as alternative to, measuring MBL concentration), particularly from
CC   activation of the lectin-complement pathway or from activity of serine
CC   proteases that are bound to MBL. The presence of both polymorphisms and
CC   C. pneumoniae is used to indicate a subgroup of patients with
CC   arteriosclerosis and severe heart disease of the coronary artery who are
CC   likely to benefit from treatment with antibiotics, native or recombinant
CC   MBL or vaccination against C. pneumoniae. MBL is a complement-activating
CC   protein that binds to C. pneumoniae and protects against infection. This
CC   sequence encodes the human MBL2 protein.
XX
SQ   Sequence 1638 BP; 454 A; 382 C; 430 G; 372 T; 0 U; 0 Other;

Query Match           100.0%;  Score 747;  DB 12;  Length 1638;
Best Local Similarity 100.0%;  Pred. No. 1.6e-207;
Matches 747;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 ATGTCCCTGTTTCCATCACTCCCTCCTCCTCCGAGTATGGTGGCAGCGTCTTACTCA 60
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Db  892 ATGTCCCTGTTTCCATCACTCCCTCCTCCTCCGAGTATGGTGGCAGCGTCTTACTCA 951

Qy   61 GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCTGCCAGTGATTGCCTGTAGCTCT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  952 GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCTGCCAGTGATTGCCTGTAGCTCT 1011

Qy  121 CCAGGCATCAACGGCTTCCAGGGAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1012 CCAGGCATCAACGGCTTCCAGGGAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 1071

Qy  181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAATTGGGGCCTCCAGGA 240
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Db 1072 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAATTGGGGCCTCCAGGA 1131

Qy  241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGGCCAAAAGGAGACCCTGAAAAAGT 300
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Db 1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGGCCAAAAGGAGACCCTGAAAAAGT 1191

Qy  301 CCGGATGTGATAGTAGCCTGGCTGCCTCAGAAGAAAAGCTCTGCAAACAGAAATGGCA 360
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Db 1192 CCGGATGTGATAGTAGCCTGGCTGCCTCAGAAGAAAAGCTCTGCAAACAGAAATGGCA 1251

Qy  361 CGTATCAAAAAGTGGCTGACCTTCTCTCGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
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Db 1252 CGTATCAAAAAGTGGCTGACCTTCTCTCGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1311

Qy  421 ACCAATGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGCC 480
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Db 1312 ACCAATGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGCC 1371

Qy  481 TCTGTGGCCACCCCAGGAAATGTGCGACGAGAATGGAGCAGCCATTCAGAATCTCATCAAGGAG 540
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Db 1372 TCTGTGGCCACCCCAGGAAATGTGCGACGAGAATGGAGCAGCCATTCAGAATCTCATCAAGGAG 1431

Qy  541 GAAGCCTTCCTGGGCATCACTGATGAAGACAGAAGGGCAGTTTGTGGATCTGACACGA 600
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Db 1432 GAAGCCTTCCTGGGCATCACTGATGAAGACAGAAGGGCAGTTTGTGGATCTGACACGA 1491

Qy  601 AATAGACTGACCTACACAAAACTGGAACGAGGGTGAACCCAACATGCTGGTTCGTGATGAA 660
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Db 1492 AATAGACTGACCTACACAAAACTGGAACGAGGGTGAACCCAACATGCTGGTTCGTGATGAA 1551

Qy  661 GATTGTGTATTGCTACTGAAAAATGCCAGTGAATGACGTCCCCTGCTCCACCTCCCAT 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1552 GATTGTGTATTGCTACTGAAAAATGCCAGTGAATGACGTCCCCTGCTCCACCTCCCAT 1611

Qy  721 CTGGCCGTCTGTGAGTTCCTATCTGA 747
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Db 1612 CTGGCCGTCTGTGAGTTCCTATCTGA 1638
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RESULT 6
ADR29056
ID   ADR29056 standard; DNA; 1638 BP.
XX
AC   ADR29056;
XX
DT   21-OCT-2004 (first entry)
XX
DE   Human MBL gene with non-structural/variant structural allele (codon 54).
XX
KW   Sepsis; septic shock; severe; MBL; mannose binding lectin; SIRS;
KW   systemic inflammatory response syndrome; innate immune defence;
KW   single nucleotide polymorphism; SNP; structural variant; regulatory;
KW   prophylaxis; sepsis syndrome; infection susceptibility;
KW   multiple organ failure; MOF; multiple organ dysfunction; acute; gene; ds;
KW   human.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
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FT   /standard_name= "Single nucleotide polymorphism"
FT   /note= "Non-structural allele"
FT   variation   396
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FT   /note= "Non-structural allele"
FT   variation   474
FT   /*tag= c
FT   /standard_name= "Single nucleotide polymorphism"
FT   /note= "Non-structural allele"
FT   variation   487
FT   /*tag= d
FT   /standard_name= "Single nucleotide polymorphism"
FT   /note= "Non-structural allele"
FT   mutation   495..500
FT   /*tag= e
FT   /note= "Optional deletion in base sequence"
FT   variation   602
FT   /*tag= f
FT   /standard_name= "Single nucleotide polymorphism"
FT   /note= "Non-structural allele"
FT   variation   753
FT   /*tag= g
FT   /standard_name= "Single nucleotide polymorphism"
FT   /note= "Non-structural allele"
FT   variation   826
FT   /*tag= h
FT   /standard_name= "Single nucleotide polymorphism"
FT   /note= "Non-structural allele"
FT   variation   1052
FT   /*tag= i
FT   /standard_name= "Single nucleotide polymorphism"
FT   /note= "Variant structural allele"
XX
PN   WO2004065626-A2.
XX
PD   05-AUG-2004.
XX
PF   16-JAN-2004; 2004WO-DK000027.
XX
PR   17-JAN-2003; 2003DK-00000042.
PR   06-MAR-2003; 2003US-0453272P.
XX
PA   (RIGS-) RIGSHOSPITALET.
PA   (KOBE-) KOBENHAVNS AMT.
XX
PI   Garred P, Madsen HO, Strom J;
XX
DR   WPI; 2004-571694/55.
XX

PT   Predicting whether an individual having Systemic Inflammatory Response
PT   Syndrome (SIRS) will develop sepsis, useful for treating sepsis,
PT   comprises determining the mannose-binding lectin (MBL) genotype or
PT   concentration of MBL.
XX
PS   Disclosure; SEQ ID NO 21; 65pp; English.
XX
CC   The invention relates to a method to determine the risk factor of a
CC   person for sepsis, severe sepsis or septic shock by correlating MBL
CC   (mannose binding lectin) genotype with a predefined risk value. It
CC   discloses the connection between the MBL genotype of an individual having
CC   SIRS (Systemic Inflammatory Response Syndrome) and the risk of developing
CC   sepsis, severe sepsis or septic shock. It shows how a decreased level of
CC   MBL and lack of functional MBL are crucial to the development of sepsis
CC   and septic shock in an individual having sepsis. A MBL is an important
CC   factor in innate immune defence. MBL single nucleotide polymorphism in
CC   the form of the structural variant (codon 54, codon 52 and codon 57) and
CC   regulatory variant (low expression and high expression) were studied.
CC   This invention discloses that the MBL gene polymorphism's causes a
CC   reduction of the MBL level, which is associated with the development and
CC   progression of sepsis in adult intensive care patients. The invention
CC   offers a service to determine whether an individual belongs to a risk
CC   group and it provides the treatment accordingly. There is an increased
CC   risk of a fatal outcome of an individual carrying MBL variant alleles. A
CC   rapid determination of MBL genotype of patients is important in
CC   identifying individuals at risk of developing sepsis, severe sepsis or
CC   septic shock. The MBL can be used for a medicament for the prevention and
CC   treatment of specified diseases. The MBL variant allele is also
CC   associated with an increased risk of death. It raises the prospective
CC   that MBL (MBL substitution) can be used in prophylaxis and treatment of
CC   sepsis syndrome. The frequency of MBL variant alleles is proportional to
CC   the severity of sepsis which indicates buffering capacity of MBL
CC   towards initial microbial replication. It is not only associated with
CC   susceptibility of infection but also allows activation of host mechanisms
CC   central to the pathophysiology of the sepsis syndrome. The invention can
CC   also predict the risk for developing multiple organ failure (MOF),
CC   multiple organ dysfunction and acute organ dysfunction of an individual
CC   having SIRS. The high risk is characterised by the presence of at least
CC   one variant structural allele of the MBL gene and or having two low
CC   expression regulatory alleles of the MBL gene in a sample. The presented
CC   sequence is the non-structural (deletion in position 495-500) and
CC   structural allele (in codon 54) of MBL from human.
XX
SQ   Sequence 1638 BP; 454 A; 382 C; 430 G; 372 T; 0 U; 0 Other;

Query Match   100.0%; Score 747; DB 13; Length 1638;
Best Local Similarity   100.0%; Pred. No. 1.6e-207;
Matches 747; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGTCCCTGTTTCCATCACTCCCTTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
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Db   892 ATGTCCCTGTTTCCATCACTCCCTTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 951

Qy   61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCTGCCAGTGATTGCCTGTAGCTCT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   952 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCTGCCAGTGATTGCCTGTAGCTCT 1011

Qy   121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCCGTGATGGCCACCAAGGGG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1012 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCCGTGATGGCCACCAAGGGG 1071

Qy   181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1072 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy   241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGAGGACCCTGGAAAAGT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGAGGACCCTGGAAAAGT 1191

Qy   301 CCGGATGGTGATAGTAGCCTGCTGCCTCAGAAAGAAAGTCTCAAACAGAAATGGCA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1192 CCGGATGGTGATAGTAGCCTGCTGCCTCAGAAAGAAAGTCTCAAACAGAAATGGCA 1251

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Qy    361  CGTATCAAAAAGTGGCTGACCTTCTCCTGGGCAAACAAGTTGGGACAAGTTCTTCCTG  420
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Db   1252  CGTATCAAAAAGTGGCTGACCTTCTCCTGGGCAAACAAGTTGGGACAAGTTCTTCCTG 1311

Qy    421  ACCAATGGTGAAATAATGACCTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC  480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1312  ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy    481  TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1372  TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy    541  GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA  600
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Db   1432  GAAGCCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1491

Qy    601  AATAGACTGACCTACACAAACTGGAACTGGAACCCAACAATGCTGGTTCTGATGAA  660
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Db   1492  AATAGACTGACCTACACAACAAACTGGAACTGGAACCCAACAATGCTGGTTCTGATGAA 1551

Qy    661  GATTGTGTATTGCTACTGAAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1552  GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1611

Qy    721  CTGGCCGTCTGTGAGTTCCCTATCTGA  747
           |||||||||||||||||||||||||||
Db   1612  CTGGCCGTCTGTGAGTTCCCTATCTGA 1638
```

XX
PI   Garred P, Madsen HO,   Strom J;
XX
DR   WPI; 2004-571694/55.
XX
PT   Predicting whether an individual having Systemic Inflammatory Response
PT   Syndrome (SIRS) will develop sepsis, useful for treating sepsis,
PT   comprises determining the mannose-binding lectin (MBL) genotype or
PT   concentration of MBL.
XX
PS   Disclosure; SEQ ID NO 24; 65pp; English.
XX

CC   The invention relates to a method to determine the risk factor of a
CC   person for sepsis, severe sepsis or septic shock by correlating MBL
CC   (mannose binding lectin) genotype with a predefined risk value. It
CC   discloses the connection between the MBL genotype of an individual having
CC   SIRS (Systemic Inflammatory Response Syndrome) and the risk of developing
CC   sepsis, severe sepsis or septic shock. It shows how a decreased level of
CC   MBL and lack of functional MBL are crucial to the development of sepsis
CC   and septic shock in an individual having sepsis. A MBL is an important
CC   factor in innate immune defence. MBL single nucleotide polymorphism in
CC   the form of the structural variant (codon 54, codon 52 and codon 57) and
CC   regulatory variant (low expression and high expression) were studied.
CC   This invention discloses that the MBL gene polymorphism's causes a
CC   reduction of the MBL level, which is associated with the development and
CC   progression of sepsis in adult intensive care patients. The invention
CC   offers a service to determine whether an individual belongs to a risk
CC   group and it provides the treatment accordingly. There is an increased
CC   risk of a fatal outcome of an individual carrying MBL variant alleles. A
CC   rapid determination of MBL genotype of patients is important in
CC   identifying individuals at risk of developing sepsis, severe sepsis or
CC   septic shock. The MBL can be used for a medicament for the prevention and
CC   treatment of specified diseases. The MBL variant allele is also
CC   associated with an increased risk of death. It raises the prospective
CC   that MBL (MBL substitution) can be used in prophylaxis and treatment of
CC   sepsis syndrome. The frequency of MBL variant alleles is proportional to
CC   the severity of sepsis which indicates lacking buffering capacity of MBL
CC   towards initial microbial replication. It is not only associated with
CC   susceptibility of infection but also allows activation of host mechanisms
CC   central to the pathophysiology of the sepsis syndrome. The invention can
CC   also predict the risk for developing multiple organ failure (MOF),
CC   multiple organ dysfunction and acute organ dysfunction of an individual
CC   having SIRS. The high risk is characterised by the presence of at least
CC   one variant structural allele of the MBL gene and or having two low
CC   expression regulatory alleles of the MBL gene in a sample. The presented
CC   sequence is the high expression regulatory allele (position 602 has a
CC   base G substitution) of MBL (mannose binding lectin) gene from human.
XX

```
Qy      1  ATGTCCCTGTTCCATCACTCCCTTCCTTCTCCGAGTATGGTGGCAGCGTCTTACTCA   60
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Db    892  ATGTCCCTGTTCCATCACTCCCTTCCTTCTCCGAGTATGGTGGCAGCGTCTTACTCA  951

Qy     61  GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    952  GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1011

Qy    121  CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCGTGATGGCACCAAGGGG  180
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Db   1012  CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCGTGATGGCACCAAGGGG 1071

Qy    181  GAACCAGGCCAAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA  240
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Db   1072  GAACCAGGCCAAGGGCTTACAGGGCTCCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy    241  AATCCAGGGCCTTCTGGTCACCAGGACCAAAAGGGCCAAAAAGGAGACCCTGAAAAAGT  300
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Db   1132  AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGGCCAAAAAGGAGACCCTGAAAAAGT 1191
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RESULT 7
ADR29059
ID   ADR29059 standard; DNA; 1638 BP.
XX
AC   ADR29059;
XX
DT   21-OCT-2004 (first entry)
XX
DE   Human MBL gene with high expression regulatory allele (602G).
XX
KW   Sepsis; septic shock; severe; MBL; mannose binding lectin; SIRS;
KW   systemic inflammatory response syndrome; innate immune defence;
KW   single nucleotide polymorphism; SNP; structural variant; regulatory;
KW   prophylaxis; sepsis syndrome; infection susceptibility;
KW   multiple organ failure; MOF; multiple organ dysfunction; acute; gene; ds;
KW   human.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
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FT   /standard_name= "Single nucleotide polymorphism"
FT   /note= "High expression regulatory allele"
FT   variation   1045
FT   /*tag= b
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PN   WO200406526-A2.
XX
PD   05-AUG-2004.
XX
PF   16-JAN-2004; 2004WO-DK000027.
XX
PR   17-JAN-2003; 2003DK-00000042.
PR   06-MAR-2003; 2003US-0453272P.
XX
PA   (RIGS-) RIGSHOSPITALET.
PA   (KOBE-) KOBENHAVNS AMT.

DR   WPI; 2004-571694/55.
XX
PT   Predicting whether an individual having Systemic Inflammatory Response
PT   Syndrome (SIRS) will develop sepsis, useful for treating sepsis,
PT   comprises determining the mannose-binding lectin (MBL) genotype or
PT   concentration of MBL.
XX
PS   Claim 5; SEQ ID NO 26; 65pp; English.
XX
CC   The invention relates to a method to determine the risk factor of a
CC   person for sepsis, severe sepsis or septic shock by correlating MBL
CC   (mannose binding lectin) genotype with a predefined risk value. It
CC   discloses the connection between the MBL genotype of an individual having
CC   SIRS (Systemic Inflammatory Response Syndrome) and the risk of developing
CC   sepsis, severe sepsis or septic shock. It shows how a decreased level of
CC   MBL and lack of functional MBL are crucial to the development of sepsis
CC   and septic shock in an individual having sepsis. A MBL is an important
CC   factor in innate immune defence. MBL single nucleotide polymorphism in
CC   the form of the structural variant (codon 54, codon 52 and codon 57) and
CC   regulatory variant (low expression and high expression) were studied.
CC   This invention discloses that the MBL gene polymorphism's causes a
CC   reduction of the MBL level, which is associated with the development and
CC   progression of sepsis in adult intensive care patients. The invention
CC   offers a service to determine whether an individual belongs to a risk
CC   group and it provides the treatment accordingly. There is an increased
CC   risk of a fatal outcome of an individual carrying MBL variant alleles. A
CC   rapid determination of MBL genotype of patients is important in
CC   identifying individuals at risk of developing sepsis, severe sepsis or
CC   septic shock. The MBL can be used for a medicament for the prevention and
CC   treatment of specified diseases. The MBL variant allele is also
CC   associated with an increased risk of death. It raises the prospective
CC   that MBL (MBL substitution) can be used in prophylaxis and treatment of
CC   sepsis syndrome. The frequency of MBL variant alleles is proportional to
CC   the severity of sepsis which indicates lacking buffering capacity of MBL
CC   towards initial microbial replication. It is not only associated with
CC   susceptibility of infection but also allows activation of host mechanisms
CC   central to the pathophysiology of the sepsis syndrome. The invention can
CC   also predict the risk for developing multiple organ failure (MOF),
CC   multiple organ dysfunction and acute organ dysfunction of an individual
CC   having SIRS. The high risk is characterised by the presence of at least
CC   one variant structural allele of the MBL gene and or having two low
CC   expression regulatory alleles of the MBL gene in a sample. The presented
CC   sequence is the low expression regulatory allele (position 602 has a base
CC   C substitution) of MBL (mannose binding lectin) gene from human.
XX
SQ   Sequence 1638 BP; 454 A; 383 C; 429 G; 372 T; 0 U; 0 Other;

Query Match   100.0%; Score 747; DB 13; Length 1638;
Best Local Similarity   100.0%; Pred. No. 1.6e-207;
Matches 747; Mismatches 0; Conservative 0; Indels 0; Gaps 0;

```
Qy     1 ATGTCCCTGTTTCCATCACTCCCTCTTCCTTCCTCCTGAGTATGGTGGCAGCGTCTTACTCA   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   892 ATGTCCCTGTTTCCATCACTCCCTCTTCCTTCCTCCTGAGTATGGTGGCAGCGTCTTACTCA  951

Qy    61 GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCTCAGTGATTGCCTGTAGCTCT  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   952 GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCTCAGTGATTGCCTGTAGCTCT 1011

Qy   121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCAGCACCAAGGGAGAAAAGGGG  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1012 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCAGCACCAAGGGAGAGAAAGGGG 1071

Qy   181 GAACCAGGCCAAGGGCTTCAGAGGGCTTACAGGGCCCCCCTGGGGCCTCCAGGA  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1072 GAACCAGGCCAAGGGCTTCAGAGGGCTTACAGGGCCCCCCTGGGGCCTCCAGGA 1131

Qy   241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGAGACCCTGAAAAAGT  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGAGACCCTGAAAAAGT 1191

Qy   301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAACAGAAATGGCA  360
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1192 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAACAGAAATGGCA 1251

Qy   361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG  420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1252 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1311

Qy   421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy   481 TCTGTGGCCACCCCCAGGAATGCTCCAGAGAATGCAGCCATTCAGAATCTCATCAAGGAG  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1372 TCTGTGGCCACCCCCAGGAATGCTCCAGAGAATGCAGCCATTCAGAATCTCATCAAGGAG 1431

Qy   541 GAAGCCTTCTGCTGGGCATCACTGATGAGAGAGACAGAGAGGGCAGTTTGTGGATCTGACAGGA  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1432 GAAGCCTTCTGCTGGGCATCACTGATGAGAGAGACAGAGAGGGCAGTTTGTGGATCTGACAGGA 1491

Qy   601 AATAGACTGACCTACCACAACTGGAACGAGGGTGAACCCAACAATGCTCGTGTTCTGATGAA  660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1492 AATAGACTGACCTACCACAACTGGAACGAGGGTGAACCCAACAATGCTCGTGTTCTGATGAA 1551

Qy   661 GATTGTGTATTGCTACTGAAAAAATGGCCAGTGACCTCCCCTGCTCCCACCTCCCAT  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1552 GATTGTGTATTGCTACTGAAAAAATGGCCAGTGACCTCCCCTGCTCCCACCTCCCAT 1611

Qy   721 CTGGCCGTCTGTGAGTTCCCTATCTGA  747
           |||||||||||||||||||||||||||
Db  1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638
```

RESULT 8
ADR29061
ID   ADR29061 standard; DNA; 1638 BP.
XX
AC   ADR29061;
XX
DT   21-OCT-2004   (first entry)
XX
DE   Human MBL low expression regulatory allele (position 602).
XX
KW   Sepsis; septic shock; severe; MBL; mannose binding lectin; SIRS;
KW   systemic inflammatory response syndrome; innate immune defence;
KW   single nucleotide polymorphism; SNP; structural variant; regulatory;
KW   prophylaxis; sepsis syndrome; infection susceptibility;
KW   multiple organ failure; MOF; multiple organ dysfunction; acute; gene; ds;
KW   human.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   variation   602
FT   /tag= a
FT   /standard_name= "Single nucleotide polymorphism"
FT   /note="Low expression regulatory allele"
XX
PN   WO2004065626-A2.
XX
PD   05-AUG-2004.
XX
PF   16-JAN-2004; 2004WO-DK000027.
XX
PR   17-JAN-2003; 2003DK-00000042.
PR   06-MAR-2003; 2003US-0453272P.
XX
PA   (RIGS-) RIGSHOSPITALET.
PA   (KOBE-) KOBENHAVNS AMT.
XX
PI   Garred P, Madsen HO, Strom J;
XX

```
        The present invention describes recombinant human mannan-binding protein
CC      (rhMBP) having a molecular weight range of 1000-1300 or 200-400 kDa (by
CC      gel filtration with detection at 280 nm). rhMBP may be used as a
CC      component of drug compositions for the inhibition of haemagglutination
CC      and prevention of infection by viruses such as influenza and HIV. The
CC      present sequence encodes hMBP (human mannan-binding protein)
XX
SQ      Sequence 3605 BP; 1055 A; 679 C; 647 G; 1224 T; 0 U; 0 Other;

        Query Match           100.0%;  Score 747;  DB 2;  Length 3605;
        Best Local Similarity 100.0%;  Pred. No. 2.3e-207;
        Matches 747;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1 ATGTCCCTGTTCCATCACTCCCTCCTTCTCCTGAGTATGGTGGCAGCGTCCTACTCA   60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTCCATCACTCCCTCCTTCTCCTGAGTATGGTGGCAGCGTCCTACTCA  125

Qy         61 GAAACTGTGACCTGTGAGATGGCCCAAAGACCTGCCCTGCCAGTGATTGCCTGTAGTCT  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAACTGTGACCTGTGAGATGGCCCAAAGACCTGCCCTGCCAGTGATTGCCTGTAGTCT  185

Qy        121 CCAGGCATCAACAGCGCTTCCAGGCAAAGATGGGCGTGATGCGTGATGCAAAGGGAGAAAAGGGG  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACAGCGCTTCCAGGCAAAGATGGGCGTGATGCGTGATGCAAAGGGAGAAAAGGGG  245

Qy        181 GAACCAGGCCAAGGGCTTACAGGCTTACAGGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTTCCAGGA  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTTACAGGCTTACAGGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTTCCAGGA  305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAGGGCCAAAACAGAAAAGT  300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAGGGCCAAAACAGAAAAGT  365

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAAATGGCA  360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAAATGGCA  425

Qy        361 CGTATCAAAAGTGGCTGACCTTCTCTGGGCAACAAGTGGGAACAAGTTCTTCCTG  420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAGTGGCTGACCTTCTCTGGGCAACAAGTGGGAACAAGTTCTTCCTG  485

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAAGGCCTTGAAGGTGTCAAGTTCCAGGCC  480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAAGGCCTTGAAGGTGTCAAGTTCCAGGCC  545

Qy        481 TCTGTGGCCACCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG  540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG  605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTGTGATCTGACAGGA  600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTGTGATCTGACAGGA  665

Qy        601 AATAGACTGACCTACACACAAACTGGAACGAGAGGTGAACCCAACAATGCTGGTTGTGATGAA  660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACACAAACTGGAACGAGAGGTGAACCCAACAATGCTGGTTGTGATGAA  725

Qy        661 GATTGTGTATTGCTACTGAAAAATGCCAGTGAATGACGTCCCTGCTCCCACCTCCAT  720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGCCAGTGAATGACGTGCCCTGCTCCCACCTCCAT  785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA  747
              |||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA  812


RESULT 10
ABN97210
ID   ABN97210 standard; DNA; 3605 BP.
XX
AC   ABN97210;
XX
```

The following is the second, rotated column of text (bottom portion, read sideways):

```
Db       1192 CCGGATGGTGATAGTAGCCTGGCTGCCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAAATGGCA 1251

Qy        361 CGTATCAAAAGTGGCTGACCTTCTCTGGGCAACAAGTGGGAACAAGTTCTTCCTG  420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1252 CGTATCAAAAGTGGCTGACCTTCTCTGGGCAACAAGTTGGGAACAAGTTCTTCCTG 1311

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAAGGCCTTGAAGGTGTCAAGTTCCAGGCC  480
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAAGGCCTTGAAGGTGTCAAGTTCCAGGCC 1371

Qy        481 TCTGTGGCCACCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG  540
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1372 TCTGTGGCCACCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA  600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1432 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1491

Qy        601 AATAGACTGACCTACACACAAACTGGAACAAACTGGAACCCAACAATGCTGGTTGTGATGAA  660
              |||||||||||||||||||||||||||||||||||||||||||||||
Db       1492 AATAGACTGACCTACACACAAACTGGAACAAACTGGAACCCAACAATGCTGGTTGTGATGAA 1551

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGAATGCTGCCCCTGCTCCCACCTCCCAT  720
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 GATTGTGTATTGCTACTGAAAAATGGCCAGTGAATGCTGCCCCTGCTCCCACCTCCCAT 1611

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA  747
              |||||||||||||||||||
Db       1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638


RESULT 9
AAZ07143
ID   AAZ07143 standard; cDNA; 3605 BP.
XX
AC   AAZ07143;
XX
DT   11-OCT-1999  (first entry)
XX
DE   Human mannan-binding protein encoding cDNA.
XX
KW   Human; mannan-binding protein; hMBP; recombinant; inhibition; infection;
KW   rhMBP; haemagglutination; influenza; HIV; primer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             66..812
FT                   /*tag= a
FT   sig_peptide     66..125
FT                   /*tag= b
FT   mat_peptide     126..809
FT                   /*tag= c
FT                   /product= "mannan-binding protein"
XX
PN   WO9937676-A1.
XX
PD   29-JUL-1999.
XX
PF   23-JUL-1998;  98WO-JP003311.
XX
PR   23-JAN-1998;  98JP-0011864.
XX
PA   (FUSO ) FUSO PHARM IND LTD.
XX
PI   Wakamiya N;
XX
DR   WPI; 1999-469114/39.
DR   P-PSDB; AAY29485.
XX
PT   Recombinant human mannan-binding protein expressed using pNOW1 vector.
XX
PS   Disclosure; Page 71-74; 91pp; Japanese.
```

DT   13-AUG-2002 (first entry)
XX
DE   Gene #3708 used to diagnose liver cancer.
XX
KW   Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW   metastatic liver tumour; cytostatic; expression profile; disease state;
KW   disease progression; drug toxicity; drug metabolism.
XX
OS   Homo sapiens.
XX
PN   WO20229103-A2.
XX
PD   11-APR-2002.
XX
PF   02-OCT-2001; 2001WO-US030589.
XX
PR   02-OCT-2000; 2000US-0237054P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX
DR   WPI; 2002-426119/45.
XX
PT   Diagnosing and detecting the progression of liver cancer, hepatocellular
PT   carcinoma or metastatic liver tumor in a patient, involves detecting the
PT   level of expression of two or more genes in a liver tissue sample.
XX
PS   Claim 1; SEQ ID NO 3708; 298pp; English.
XX
CC   The invention relates to a novel method for diagnosing and detecting the
CC   progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC   tumour in a patient, and differentiating metastatic liver cancer from
CC   expression of two or more genes represented in ABN93503-ABN97455 in a
CC   tissue sample. The method of the invention has hepatotropic, and
CC   cytostatic activity. The method is useful for diagnosing and detecting
CC   the progression of liver cancer, hepatocellular carcinoma and metastatic
CC   liver carcinoma in a patient. The method is useful for identifying
CC   expression profiles which serve as useful diagnostic markers as well as
CC   markers that can be used to monitor disease states, disease progression
CC   drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 3605 BP; 1055 A; 679 C; 1224 T; 0 U; 0 Other;

Query Match   100.0%; Score 747; DB 6; Length 3605;
Best Local Similarity 100.0%; Pred. No. 2.3e-207;
Matches 747; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATGTCCCTGTTTCCATCACTCCCTCCTTCCTTCCTGAGTATGGTGGCAGCCGTCTTACTCA 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 ATGTCCCTGTTTCCATCACTCCCTCCTTCCTTCCTGAGTATGGTGGCAGCCGTCTTACTCA 125

Qy   61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCCAGTGATTGCCTGTAGCTCT 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCCAGTGATTGCCTGTAGCTCT 185

Qy   121 CCAGGCATCAACGGCTTCCAGGCAAAGATGGGCGTGATGGCCACCAAGGGAGAAAAGGGG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 CCAGGCATCAACGGCTTCCAGGCAAAGATGGGCGTGATGGCCACCAAGGGAGAAAAGGGG 245

Qy   181 GAACCAGGCCAAGGGCTTACAGGGCCCCCCCTGGAAAGTTGGGGGCCTCCAGGA 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246 GAACCAGGCCAAGGGCTCAGAGGCTTACACGGCCCCCCCTGGAAAGTTGGGGGCCTCCAGGA 305

Qy   241 AATCCAGGGCTTCTGGGTCACCAGGACCAAAGGGCCAAAAGGACACCCTGGAAAAGT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 AATCCAGGGCTTCTGGGTCACCAGGACCAAAGGGCCAAAAGGAGACCCCTGGAAAAAGT 365

Qy   301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAGAAAGTCTGCAAACAGAAATGGCA 360

Db   366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAGAAAGTCTGCAAACAGAAATGGCA 425
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   361 CGTATCAAAAAGTGGCTGACCTTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426 CGTATCAAAAAGTGGCTGACCTTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy   421 ACCAATGGTGAAATAATGACCTTTGAAAAGTGAAGGCCTTGTGTCAAGTTCCAGGCC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486 ACCAATGGTGAAATAATGACCTTTGAAAAGTGAAGGCCTTGTGTCAAGTTCCAGGCC 545

Qy   481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy   541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTTGGATCTGACAGGA 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665

Qy   601 AATAGACTGACCTACACAACAACTGGAACCCAACAATGCTGGTTCTGATGAA 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666 AATAGACTGACCTACACAACAACTGGAACCCAACAATGCTGGTTCTGATGAA 725

Qy   661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCCAT 785

Qy   721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
             ||||||||||||||||||||||||||||
Db   786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812

RESULT 11
ADI20099
ID   ADI20099 standard; DNA; 3605 BP.
XX
AC   ADI20099;
XX
DT   22-APR-2004 (first entry)
XX
DE   DNA sequence #1 related to the invention.
XX
KW   anti-human immunodeficiency virus; HIV; mannose binding protein; MBP; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004002511-A1.
XX
PD   08-JAN-2004.
XX
PF   30-JUN-2003; 2003WO-JP008259.
XX
PR   28-JUN-2002; 2002JP-00189534.
XX
PA   (FUSO) FUSO PHARM IND LTD.
XX
PI   Wakamiya N, Ohtani K, Sakamoto T, Keshi H, Kishi Y;
XX
DR   WPI; 2004-082879/08.
XX
PT   Anti-human immunodeficiency virus (HIV) agent comprising a mannose
PT   binding protein for treatment of HIV infection.
XX
PS   Disclosure; SEQ ID NO 1; 44pp; Japanese.
XX
CC   The present invention relates to anti-human immunodeficiency virus (HIV)
CC   agent comprises a mannose binding protein (MBP). For use in the treatment
CC   of HIV. The present sequence represents a DNA sequence related to the
CC   invention.
XX
SQ   Sequence 3605 BP; 1055 A; 679 C; 1224 T; 0 U; 0 Other;

Query Match   100.0%; Score 747; DB 12; Length 3605;

```
PN   US2004023276-A1.
XX
PD   05-FEB-2004.
XX
PF   02-MAY-2003; 2003US-0429160.
XX
PR   03-MAY-2002; 2002US-0377714P.
XX
PA   (WARD/)  WARD T R.
PA   (MAOM/)  MAO M.
PA   (LINS/)  LINSLEY P S.
PA   (LUND/)  LUND E.
XX
PI   Ward TR, Mao M, Linsley PS, Lund E;
XX
DR   WPI; 2004-224687/21.
DR   P-PSDB; ADJ45527.
XX
PT   New purified Liver X receptor (LXR) nucleic acids, useful for diagnosing
PT   a disease involving LXR activity, such as cholesterol gallstones,
PT   atherosclerosis, lipid storage diseases, obesity, diabetes, or
PT   hypercholesterolemia.
XX
PS   Example 1; SEQ ID NO 57; 141pp; English.
XX
CC   The invention describes a purified nucleic acid comprising a fully
CC   defined sequence of 1586 bp (SEQ ID NO: 1) as given in the specification,
CC   or its complement. The methods and compositions are useful for diagnosing
CC   a disease or disorder involving LXR (liver X receptor) activity in a
CC   sample by detecting an increase or decrease in the transcript level
CC   relative to the amount present in an analogous sample from a subject not
CC   having the disease or disorder or not subjected to therapy, wherein the
CC   disease or disorder is cholesterol gallstones, atherosclerosis, lipid
CC   storage diseases, obesity, diabetes, or hypercholesterolaemia. They are
CC   also used to identify a compound that changes LXR activity, wherein the
CC   compound changes the estimated level of LXR activity in a sample from the
CC   subject contacted with the compound relative to the estimated level of
CC   LXR activity in an analogous sample from the subject not contacted with
CC   the compound. This sequence encodes an LXR regulated protein.
XX
SQ   Sequence 3605 BP; 1055 A; 679 C; 647 G; 1224 T; 0 U; 0 Other;

Query Match            100.0%;  Score 747;  DB 12;  Length 3605;
Best Local Similarity  100.0%;  Pred. No. 2.3e-207;
Matches  747;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 ATGTCCCTGTTCCATCACTCCCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 ATGTCCCTGTTCCATCACTCCCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA  125

Qy   61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGAGTGTCCTGTAGCTCT   120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGAGTGTCCTGTAGCTCT   185

Qy  121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG   180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG   245

Qy  181 GAACCAGGCCAAGGGCTTACAGGGCCCCCCCTGGAAAGTTGGGGCCTCCAGGA   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  246 GAACCAGGCCAAGGGCTTACAGGGCCCCCCCTGGAAAGTTGGGGCCTCCAGGA   305

Qy  241 AATCCAGGGCCTTCGGGTCACCAGGACCAAAAGGAGACCCTGGAAAAAGT   300
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  306 AATCCAGGGCCTTCGGGTCACCAGGACCAAAAGGAGACCCTGGAAAAAGT   365

Qy  301 CCGGATGGTGATAGTAGCCTGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA   360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  366 CCGGATGGTGATAGTAGCCTGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA   425

Qy  361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGACAACAAGTTCTTCCTG   420
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGACAACAAGTTCTTCCTG   485
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Best Local Similarity  100.0%;  Pred. No. 2.3e-207;  Indels  0;  Gaps  0;
Matches  747;  Conservative  0;  Mismatches  0;

Qy    1 ATGTCCCTGTTCCATCACTCCCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   66 ATGTCCCTGTTCCATCACTCCCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA  125

Qy   61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGAGTGTCCTGTAGCTCT   120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGAGTGTCCTGTAGCTCT   185

Qy  121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG   180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG   245

Qy  181 GAACCAGGCCAAGGGCTTACAGGGCCCCCCCTGGAAAGTTGGGGCCTCCAGGA   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  246 GAACCAGGCCAAGGGCTTACAGGGCCCCCCCTGGAAAGTTGGGGCCTCCAGGA   305

Qy  241 AATCCAGGGCCTTCGGGTCACCAGGACCAAAAGGAGACCCTGGAAAAAGT   300
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  306 AATCCAGGGCCTTCGGGTCACCAGGACCAAAAGGAGACCCTGGAAAAAGT   365

Qy  301 CCGGATGGTGATAGTAGCCTGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA   360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  366 CCGGATGGTGATAGTAGCCTGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA   425

Qy  361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTCTTCCTG   420
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTCTTCCTG   485

Qy  421 ACCAATGTGAAATAATGACCTTTGAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC   480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  486 ACCAATGTGAAATAATGACCTTTGAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC   545

Qy  481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGAGCCATTCAGAATCTCATCAAGGAG   540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGAGCCATTCAGAATCTCATCAAGGAG   605

Qy  541 GAAGCCTTCCTGTGGCATCACTGATGAGAAGACAGAGAGGGCAGTTTGTGGATCTGACAGGA   600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  606 GAAGCCTTCCTGTGGCATCACTGATGAGAAGACAGAGAGGGCAGTTTGTGGATCTGACAGGA   665

Qy  601 AATAGAGACTGACCTACACAACAAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA   660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  666 AATAGAGACTGACCTACACAACAAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA   725

Qy  661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACTTCCCAT   720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACTTCCCAT   785

Qy  721 CTGGCCGTCTGTGAGTTCCCTATCTGA  747
          |||||||||||||||||||||||||||
Db  786 CTGGCCGTCTGTGAGTTCCCTATCTGA  812

RESULT 12
ADJ45526
ID   ADJ45526 standard; cDNA; 3605 BP.
XX
AC   ADJ45526;
XX
DT   06-MAY-2004  (first entry)
XX
DE   cDNA encoding LXR-ligand induced transcript seq id 57.
XX
KW   LXR; liver X receptor; cholesterol; gallstone; atherosclerosis;
KW   lipid storage disease; obesity; diabetes; hypercholesterolaemia;
KW   LXR-ligand induced 1; LXRlI1; human; LXR-ligand induced transcript;
KW   LXR regulated gene; ss; gene.
XX
OS   Homo sapiens.
XX
```

The invention relates to a method to determine the risk factor of a
person for sepsis, severe sepsis or septic shock by correlating MBL
(mannose binding lectin) genotype with a predefined risk value. It
discloses the connection between the MBL genotype of an individual having
SIRS (Systemic Inflammatory Response Syndrome) and the risk of developing
sepsis, severe sepsis or septic shock. It shows how a decreased level of
MBL and lack of functional MBL are crucial to the development of sepsis
and septic shock in an individual having sepsis. A MBL is an important
factor for innate immune defence. MBL single nucleotide polymorphism in
the form of the structural variant (codon 54, codon 52 and codon 57) and
regulatory variant (low expression and high expression) were studied.
This invention discloses that the MBL gene polymorphism's causes a
reduction of the MBL level, which is associated with the development and
progression of sepsis in adult intensive care patients. The invention
offers a service to determine whether an individual belongs to a risk
group and it provides the treatment accordingly. There is an increased
risk of a fatal outcome of an individual carrying MBL variant alleles. A
rapid determination of MBL genotype of patients is important in
identifying individuals at risk of developing sepsis, severe sepsis or
septic shock. The MBL can be used for a medicament for the prevention and
treatment of specified diseases. The MBL variant allele is also
associated with an increased risk of death. It raises the prospective
that MBL (MBL substitution) can be used in prophylaxis and treatment of
sepsis syndrome. The frequency of MBL variant alleles is proportional to
the severity of sepsis which indicates lacking buffering capacity of MBL
towards initial microbial replication. It is not only associated with
susceptibility of infection but also allows activation of host mechanisms
central to the pathophysiology of the sepsis syndrome. The invention can
also predict the risk for developing multiple organ failure (MOF),
multiple organ dysfunction and acute organ dysfunction of an individual
having SIRS. The high risk is characterised by the presence of at least
one variant structural allele of the MBL gene and or having two low
expression regulatory alleles of the MBL gene in a sample. The presented
sequence is the variant structural allele (in codon 57) of MBL (mannose
binding lectin) gene from human.

Sequence 1632 BP; 448 A; 381 C; 429 G; 374 T; 0 U; 0 Other;

Query Match   99.8%; Score 745.4; DB 13; Length 1632;
Best Local Similarity   99.9%; Pred. No. 4.7e-207;
Matches 746;   Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy      1 ATGTCCCTGTTTCATCACTCCCCTCCTCCTCCTCCTCGAGTATGGTGGCAGGCTCTTACTCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    886 ATGTCCCTGTTTCATCACTCCCCTCCTCCTCCTCCTCGAGTATGGTGGCAGGCTCTTACTCA 945

Qy     61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGAGTCTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    946 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGAGTCTCT 1005

Qy    121 CCAGGCATCAACGGCTTCCAGGCAAAGATGGGCCAGTGCACCAAGGGAGAAGAAAAGGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1006 CCAGGCATCAACGGCTTCCAGGCAAAGATGGGCCAGTGCACCAAGGGAGAAGAAAAGGGG 1065

Qy    181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGG 240
          |||||||||||||||||||||||||||||||
Db   1066 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGG 1125

Qy    241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAGGGCCAAAAAAGT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1126 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAGGGCCAAAAAAGT 1185

Qy    301 CCGGATGGTGATAGTAGCCTGGCTGCCAGAAAGAAAAAGCTCTGCAAACAGAAATCGCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1186 CCGGATGGTGATAGTAGCCTGGCTGCCAGAAAGAAAAAGCTCTGCAAACAGAAATCGCA 1245

Qy    361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGACCAAGCAAGTTCTTCCTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1246 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGACCAAGCAAGTTCTTCCTG 1305

Qy    421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTCAAGTTCCAGGCC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTCAAGTTCCAGGCC 545

Qy    481 TCTGTGGCCACCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAGGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 TCTGTGGCCACCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGAG 605

Qy    541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTGTGGATCGACAGGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTGTGGATCGACAGGA 665

Qy    601 AATAGACTGACCTACCAACCTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGGTTCTGATGAA 660
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 AATAGACTGACCTACACCAACCTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGGTTCTGATGAA 725

Qy    661 GATTGTGTATTGCTACTGAAAAATGCCAGTGGAATGACGTCCCCTGCTCCCACCTCCAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 GATTGTGTATTGCTACTGAAAAATGCCAGTGGAATGACGTCCCCTGCTCCCACCTCCCAT 785

Qy    721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
          |||||||||||||||||||||||||||
Db    786 CTGGCCCGTCTGTGAGTTCCCTATCTGA 812
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RESULT 13
ADR29057
ID   ADR29057 standard; DNA; 1632 BP.
XX
AC   ADR29057;
XX
DT   21-OCT-2004 (first entry)
XX
DE   Human MBL gene with variant structural allele (in codon 57).
XX
KW   Sepsis; septic shock; severe; MBL; mannose binding lectin; SIRS;
KW   systemic inflammatory response syndrome; innate immune defence;
KW   single nucleotide polymorphism; SNP; structural variant; regulatory;
KW   prophylaxis; sepsis syndrome; infection susceptibility; acute; gene; ds;
KW   multiple organ failure; MOF; multiple organ dysfunction.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   variation   1055
FT   /tag= a
FT   /standard_name= "Single nucleotide polymorphism"
FT   /note="Variant structural allele"
XX
PN   WO2004065626-A2.
XX
PD   05-AUG-2004.
XX
PF   16-JAN-2004; 2004WO-DK000027.
XX
PR   17-JAN-2003; 2003DK-00000042.
PR   06-MAR-2003; 2003US-0453272P.
XX
PA   (RIGS-) RIGSHOSPITALET.
PA   (KOBE-) KOBENHAVNS AMT.
XX
PI   Garred P, Madsen HO, Strom J;
XX
DR   WPI; 2004-571694/55.
XX
PT   Predicting whether an individual having Systemic Inflammatory Response
PT   Syndrome (SIRS) will develop sepsis, useful for treating sepsis,
PT   comprises determining the mannose-binding lectin (MBL) genotype or
PT   concentration of MBL.
XX
PS   Claim 3; SEQ ID NO 22; 65pp; English.

CC   (mannose binding lectin) genotype with a predefined risk value. It
CC   discloses the connection between the MBL genotype of an individual having
CC   SIRS (Systemic Inflammatory Response Syndrome) and the risk of developing
CC   sepsis, severe sepsis or septic shock. It shows how a decreased level of
CC   MBL and lack of functional MBL are crucial to the development of sepsis
CC   and septic shock in an individual having sepsis. A MBL is an important
CC   factor in innate immune defence. MBL single nucleotide polymorphism in
CC   the form of the structural variant (codon 54, codon 52 and codon 57) and
CC   regulatory variant (low expression and high expression) were studied.
CC   This invention discloses that the MBL gene polymorphism's causes a
CC   reduction of the MBL level, which is associated with the development and
CC   progression of sepsis in adult intensive care patients. The invention
CC   offers a service to determine whether an individual belongs to a risk
CC   group and it provides the treatment according. There is an increased
CC   risk of a fatal outcome of an individual carrying MBL variant alleles. A
CC   rapid determination of MBL genotype of patients is important in
CC   identifying individuals at risk of developing sepsis, severe sepsis or
CC   septic shock. The MBL can be used for a medicament for the prevention and
CC   treatment of specified diseases. The MBL variant allele is also
CC   associated with an increased risk of death. It raises the prospective
CC   that MBL (MBL substitution) can be used in prophylaxis and treatment of
CC   sepsis syndrome. The frequency of MBL variant alleles is proportional to
CC   the severity of sepsis which indicates lacking buffering capacity of MBL
CC   towards initial microbial replication. It is not only associated with
CC   susceptibility of infection but also allows activation of host mechanisms
CC   central to the pathophysiology of the-sepsis syndrome. The invention can
CC   also predict the risk for developing multiple organ failure (MOF),
CC   multiple organ dysfunction and acute organ dysfunction of an individual
CC   having SIRS. The high risk is characterised by the presence of at least
CC   one variant structural allele of the MBL gene and or having two low
CC   expression regulatory alleles of the MBL gene in a sample. The presented
CC   sequence is human MBL gene with variant structural allele (in codon 54).
XX
SQ   Sequence 1638 BP; 455 A; 382 C; 429 G; 372 T; 0 U; 0 Other;

Query Match   99.8%;   Score 745.4;   DB 13;   Length 1638;
Best Local Similarity   99.9%;   Pred. No. 4.7e-207;
Matches 746;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy   1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCGAGTATGGTGGCAGCGTCTTACTCA 60
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Db   892 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCGAGTATGGTGGCAGCGTCTTACTCA 951

Qy   61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCCAGTGATTGCCTGTAGTCT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   952 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCCAGTGATTGCCTGTAGTCT 1011

Qy   121 CCAGGCATCAACGGCTTCCAGCAAGATGGCGTGATGGCCAACGGAGCAAGAGGG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1012 CCAGGCATCAACGGCTTCCAGCAAGATGGCGTGATGGCCAACGGAGCAAGAGGG 1071

Qy   181 GAACCAGGCCAAGGGCTTACAGGAGCTTACAGGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1072 GAACCAGGCCAAGGGCTTACAGGAGCTTACAGGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy   241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGGCCAAAAAGGAGACCCTGGAAAAGT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGGCCAAAAAGGAGACCCTGGAAAAGT 1191

Qy   301 CCGGATGGTGATAGTAGCCTGGCTGCCTCCAGAAGAAGAAAAGCTCTGCAAACAGAAATGGCA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1192 CCGGATGGTGATAGTAGCCTGGCTGCCTCCAGAAGAAGAAAAGCTCTGCAAACAGAAATGGCA 1251

Qy   361 CGTATCAAAAGTGGCTGACCTTCTCTCGGGCAAACAAGTTGGAACAAGTTCTTCCTG 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1252 CGTATCAAAAGTGGCTGACCTTCTCTCGGGCAAACAAGTTGGAACAAGTTCTTCCTG 1311

Qy   421 ACCAATGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTCAAGTTCCAGGCC 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1312 ACCAATGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTCAAGTTCCAGGCC 1371

Qy   481 TCTGTGGCCACCCCCAGGAAATCTGAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1306 ACCAATGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTCAAGTTCCAGGCC 1365
Qy   481 TCTGTGGCCACCCCCAGGAAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1366 TCTGTGGCCACCCCCAGGAAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1425

Qy   541 GAAGCCTTCCTGGCATCACTGATGAAGACAGAAGGGCAGTTGTGGATCTGACACGGA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1426 GAAGCCTTCCTGGCATCACTGATGAAGACAGAAGGGCAGTTGTGGATCTGACACGGA 1485

Qy   601 AATAGACTGACCTACACAAACTGGAACTGGAACCCAACAATGCTGGTTCTGATGAA 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1486 AATAGACTGACCTACACAAACTGGAACTGGAACCCAACAATGCTGGTTCTGATGAA 1545

Qy   661 GATTGTGTATTGCTACTGAAAAATGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1546 GATTGTGTATTGCTACTGAAAAATGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1605

Qy   721 CTGGCCGGTCGTGTGAGTTCCCTATCTGA 747
            |||||||||||||||||||||||||||||
Db   1606 CTGGCCGGTCGTGTGAGTTCCCTATCTGA 1632

RESULT 14
ADR29058
ID   ADR29058 standard; DNA; 1638 BP.
XX
AC   ADR29058;
XX
DT   21-OCT-2004 (first entry)
XX
DE   Human MBL gene with variant structural allele (in codon 54).
XX
KW   Sepsis; septic shock; severe; MBL; mannose binding lectin; SIRS;
KW   systemic inflammatory response syndrome; innate immune defence;
KW   single nucleotide polymorphism; SNP; structural variant; regulatory;
KW   prophylaxis; sepsis syndrome; infection susceptibility;
KW   multiple organ failure; MOF; multiple organ dysfunction; acute; gene; ds;
KW   human.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   variation   1052
FT   /*tag= a
FT   /standard_name= "Single nucleotide polymorphism"
FT   /note= "Variant structural allele"
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PN   WO2004065526-A2.
XX
PD   05-AUG-2004.
XX
PF   16-JAN-2004; 2004WO-DK000027.
XX
PR   17-JAN-2003; 2003DK-00000042.
PR   06-MAR-2003; 2003US-0453272P.
XX
PA   (RIGS-) RIGSHOSPITALET.
PA   (KOBE-) KOBENHAVNS AMT.
XX
PI   Garred P, Madsen HO, Strom J;
XX
DR   WPI; 2004-571694/55.
XX
PT   Predicting whether an individual having Systemic Inflammatory Response
PT   Syndrome (SIRS) will develop sepsis, useful for treating sepsis,
PT   comprises determining the mannose-binding lectin (MBL) genotype or
PT   concentration of MBL.
XX
PS   Claim 3; SEQ ID NO 23; 65pp; English.
XX
CC   The invention relates to a method to determine the risk factor of a
CC   person for sepsis, severe sepsis or septic shock by correlating MBL

CC (mannose binding lectin) genotype with a predefined risk value. It
CC discloses the connection between the MBL genotype and the risk of having
CC SIRS (Systemic Inflammatory Response Syndrome) and the risk of developing
CC sepsis, severe sepsis or septic shock. It shows how a decreased level of
CC MBL and lack of functional MBL are crucial to the development of sepsis
CC and septic shock in an individual having sepsis. A MBL is an important
CC factor in innate immune defence. MBL single nucleotide polymorphism in
CC the form of the structural variant (codon 54, codon 52 and codon 57) and
CC regulatory variant (low expression and high expression) were studied.
CC This invention discloses that the MBL gene polymorphism's causes a
CC reduction of the MBL level, which is associated with the development and
CC progression of sepsis in adult intensive care patients. The invention
CC offers a service to determine whether an individual belongs to a risk
CC group and it provides the treatment accordingly. There is an increased
CC risk of a fatal outcome of an individual carrying MBL variant alleles. A
CC rapid determination of MBL genotype of patients is important in
CC identifying individuals at risk of developing sepsis, severe sepsis or
CC septic shock. The MBL can be used for a medicament for the prevention and
CC treatment of specified diseases. The MBL variant allele is also
CC associated with an increased risk of death. It raises the prospective
CC that MBL (MBL substitution) can be used in prophylaxis and treatment of
CC sepsis syndrome. The frequency of MBL variant alleles is proportional to
CC the severity of sepsis which indicates lacking buffering capacity of MBL
CC towards initial microbial replication. It is not only associated with
CC susceptibility of infection but also allows activation of host mechanisms
CC central to the pathophysiology of the sepsis syndrome. The invention can
CC also predict the risk for developing multiple organ failure (MOF)
CC multiple organ dysfunction and acute organ dysfunction of an individual
CC having SIRS. The high risk is characterised by the presence of at least
CC one variant structural allele of the MBL gene and or having two low
CC expression regulatory alleles of the MBL gene in a sample. The presented
CC sequence is the human MBL gene with non-structural/variant structural
CC allele (in codon 52).
XX
SQ Sequence 1638 BP; 454 A; 380 C; 431 G; 373 T; 0 U; 0 Other;

Query Match   99.8%;   Score 745.4;   DB 13;   Length 1638;
Best Local Similarity   99.9%;
Matches   746;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   0;

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Qy    1 ATGTCCCCTGTTTCCATCACTCCCTTCCTCCTGAGTAGTGGTGCAGCGTCTTACTCA   60
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Db  892 ATGTCCCCTGTTTCCATCACTCCCTTCCTCCTGAGTAGTGGTGCAGCGTCTTACTCA  951

Qy   61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCTGCCTGCAGTGATTGCCTGTAGCTCT  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  952 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCTGCCTGCAGTGATTGCCTGTAGCTCT 1011

Qy  121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCCGTGATGCGCACCAAGGGAGAAAGGGG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1012 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCCGTGATGCGCACCAAGGGAGAAAGGGG 1071

Qy  181 GAACCAGGCCAAGGGCTTCAGAGGGCTTACAGGGCCCCCTGAAAGTTGGGGCCTCCAGGA  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1072 GAACCAGGCCAAGGGCTTCAGAGGGCTTACAGGGCCCCCTGAAAGTTGGGGCCTCCAGGA 1131

Qy  241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGACCAAAAAGGAGACCCTGGAAAAAGT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGACCAAAAAGGAGACCCTGGAAAAAGT 1191

Qy  301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAGAAGAAGAAAGTCTCGCAAACAGAAATGCA  360
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Db 1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638
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RESULT 15
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ID   ADR29060   standard; DNA; 1638 BP.
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AC   ADR29060;
XX
DT   21-OCT-2004   (first entry)
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DE   Human MBL gene with non-structural/variant structural allele (codon 52).
XX
KW   Sepsis; septic shock; severe; MBL; mannose binding lectin; SIRS;
KW   systemic inflammatory response syndrome; innate immune defence;
KW   single nucleotide polymorphism; SNP; structural variant; regulatory;
KW   prophylaxis; sepsis syndrome; infection susceptibility; acute; gene; ds;
KW   human.
XX
OS   Homo sapiens.
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FT   /note= "Non-structural allele"
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FT   /note= "Variant structural allele"
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XX
PD   05-AUG-2004.
XX
PF   16-JAN-2004; 2004WO-DK000027.
XX
PR   17-JAN-2003; 2003DK-00000042.
PR   06-MAR-2003; 2003US-0453272P.
XX
PA   (RIGS-) RIGSHOSPITALET.
PA   (KOBE-) KOBENHAVNS AMT.
XX
PI   Garred P, Madsen HO, Strom J;
XX
DR   WPI; 2004-571694/55.
XX
PT   Predicting whether an individual having Systemic Inflammatory Response
PT   Syndrome (SIRS) will develop sepsis, useful for treating sepsis,
PT   comprises determining the mannose-binding lectin (MBL) genotype or
PT   concentration of MBL.
XX
PS   Claim 3; SEQ ID NO 25; 65pp; English.
XX
CC   The invention relates to a method to determine the risk factor of a
CC   person for sepsis, severe sepsis or septic shock by correlating MBL

```
Db            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1372 TCTGTGTGGCCACCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy     541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
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Qy     601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
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Db    1492 AATAGACTGACCTACACAACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1551

Qy     661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
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Qy     721 CTGGCCGTCGTGTGAGTTCCCTATCTGA 747
            ||||||||||||||||||||||||||||
Db    1612 CTGGCCGTCGTGTGAGTTCCCTATCTGA 1638
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Search completed: June 20, 2005, 16:01:54
Job time : 545 secs

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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:     June 19, 2005, 17:17:35 ; Search time 184 Seconds
                                (without alignments)
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Title:         US-10-054-536-2
Perfect score: 747
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Scoring table: IDENTITY_NUC
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Searched:      1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:     2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                         SUMMARIES
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1	747	100.0	900	3	US-09-198-603C-1	Sequence 1, Appli
2	747	100.0	1340	4	US-09-949-016-3499	Sequence 3499, Ap
3	747	100.0	3605	4	US-09-949-016-36	Sequence 36, Appl
4	374	50.1	8093	4	US-09-949-016-15241	Sequence 15241, A
5	374	50.1	10320	4	US-09-949-016-11778	Sequence 11778, A
6	204.4	27.4	1211	3	US-09-198-603C-25	Sequence 25, Appl
7	188	25.2	601	4	US-09-949-016-18336	Sequence 18336, A
8	188	25.2	601	4	US-09-949-016-124315	Sequence 124315,
9	126	16.9	714	3	US-09-198-603C-26	Sequence 26, Appl
c 10	74	9.9	601	4	US-09-949-016-18337	Sequence 18337, A
c 11	74	9.9	601	4	US-09-949-016-124316	Sequence 124316,
c 12	73.4	9.8	1558	3	US-09-198-603C-24	Sequence 24, Appl
c 13	72	9.6	601	4	US-09-949-016-18342	Sequence 18342, A
c 14	72	9.6	601	4	US-09-949-016-124321	Sequence 124321,
15	67.6	9.0	885	1	US-08-365-103B-3	Sequence 3, Appli
16	67.6	9.0	924	1	US-08-365-103B-5	Sequence 5, Appli
17	67.6	9.0	1005	1	US-08-365-103B-1	Sequence 1, Appli
18	63.4	8.5	747	4	US-09-949-016-741	Sequence 741, App
19	62.8	8.4	369	3	US-09-535-521-24	Sequence 24, Appl
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c 25	62.8	8.4	423	3	US-09-535-521-13	Sequence 13, Appl
c 26	62.8	8.4	423	3	US-09-535-521-15	Sequence 15, Appl
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c 28	62.8	8.4	561	3	US-09-535-521-18	Sequence 18, Appl
c 29	62.8	8.4	624	3	US-09-535-521-19	Sequence 19, Appl
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c 34	62.8	8.4	2851	3	US-09-535-521-3	Sequence 2610, Ap
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36	61.8	8.3	1412	4	US-09-949-016-3187	Sequence 3188, Ap
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38	60.2	8.1	6288	4	US-09-949-016-12483	Sequence 14929, A
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                          ALIGNMENTS

RESULT 1
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 ; Sequence 1, Application US/09198603C
 ; Patent No. 6337193
 ; GENERAL INFORMATION:
 ;  APPLICANT: TULLY, Raymond E.
 ;  APPLICANT: CALTAGIRONE, G. Thomas
 ;  APPLICANT: MOYER, Shawn S.
 ;  APPLICANT: RONNING, Michael T.
 ;  TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC
 ;  TITLE OF INVENTION: YEAST
 ;  FILE REFERENCE: A7290
 ;  CURRENT APPLICATION NUMBER: US/09/198,603C
 ;  CURRENT FILING DATE: 1998-11-24
 ;  NUMBER OF SEQ ID NOS: 26
 ;  SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ;  LENGTH: 900
 ;  TYPE: DNA
 ;  ORGANISM: Human
US-09-198-603C-1

Query Match             100.0%;  Score 747;  DB 3;  Length 900;
Best Local Similarity   100.0%;  Pred. No. 2.1e-227;
Matches  747;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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RESULT 2
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; Sequence 3499, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3499
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3499

Query Match   100.0%;   Score 747; DB 4; Length 1340;
Best Local Similarity 100.0%;   Pred. No. 2.6e-227;
Matches 747; Conservative   0; Mismatches   0; Indels 0; Gaps 0;

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Right column:

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Qy   241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
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Qy   301 CCGGATGGTGATAGTAGCCTGCGCTGCGCTCAGAAGAAAAGCTGCAAACAGAGAAATGGCA 360
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Db   366 CCGGATGGTGATAGTAGCCTGCGCTGCGCTCAGAAGAAAAGCTGCAAACAGAGAAATGGCA 425

Qy   361 CGTATCAAAAAGTGCTGACCTTCTCTCTCGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
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Qy   661 GATTGTGTATTGCTACTGAAAAATGCCAGTGGAATGAGCGTCCCCTATCTGA 720
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Qy   721 CTGGCCGTCGTGTGAGTTCCCTATCTGA 747
             ||||||||||||||||||||||||||||
Db   786 CTGGCCGTCGTGTGAGTTCCCTATCTGA 812
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RESULT 3
US-09-949-016-36
; Sequence 36, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 3605
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-36

Query Match   100.0%;   Score 747; DB 4; Length 3605;
Best Local Similarity 100.0%;   Pred. No. 4.6e-227;
Matches 747; Conservative   0; Mismatches   0; Indels 0; Gaps 0;

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Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5371 GCATCACTGATGAGAAGACAGAGGGCAGTTTGTGGATCTGACAGGAAATAGACTGACCT 5430

Qy    614 ACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGC 673
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Qy    674 TACTGAAAAATGGCCAGTGGAATGACGTCCCGTCCCACCTCCACCTCCACCTCGGCCGTCTG 733
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5491 TACTGAAAAATGGCCAGTGGAATGACGTCCCGTCCCACCTCCACCTCCACCTCGGCCGTCTG 5550

Qy    734 AGTTCCCTATCTGA 747
          ||||||||||||||
Db   5551 AGTTCCCTATCTGA 5564
```

RESULT 5
US-09-949-016-11778
; Sequence 11778, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11778
; LENGTH: 10320
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11778

Query Match 50.1%; Score 374; DB 4; Length 10320;
Best Local Similarity 100.0%; Pred. No. 5.5e-108;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    374 GGCTGACCTTCTCTCTCGGGCAAACAAGTTGGAACAAGTTCTTCCTGACCAATGGTGAAA 433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5191 GGCTGACCTTCTCTCTCGGGCAAACAAGTTGGAACAAGTTCTTCCTGACCAATGGTGAAA 5250

Qy    434 TAATGACCTTTGAAAAAGTGAAGGCCTTCAGGTTCAAGTTCAAGTTCAGGCCTCGTGCCACCC 493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5251 TAATGACCTTTGAAAAAGTGAAGGCCTTCAGGTTCAAGTTCAAGTTCAGGCCTCGTGCCACCC 5310

Qy    494 CCAGGAATGCTGCAGAGAATGAGACCATTCATCAAGGAGAAGGAAGCCTTCCTGG 553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5311 CCAGGAATGCTGCAGAGAATGAGACCATTCATCAAGGAGAAGGAAGCCTTCCTGG 5370
```

```
Db    126 GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 CCAGGCCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAGGGG 180

Db    186 CCAGGCCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAGGGG 245
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181 GAACCAGGCCAAGGGCTCAGAGGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240

Db    246 GAACCAGGCCAAGGGCTCAGAGGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241 AATCCAGGGCCTTCGGTCACCAGGACCAAAGGGCAAAAGGAGACCCTGGAAAAAGT 300

Db    306 AATCCAGGGCCTTCGGTCACCAGGACCAAAGGGCAAAAGGAGACCCTGGAAAAAGT 365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301 CCGGATGGTGATAGTAGCCTGCTGCCTCAGAAAGAAAAGCTTCGCAAACAGAAATGGCA 360

Db    366 CCGGATGGTGATAGTAGCCTGCTGCCTCAGAAAGAAAAGCTTCGCAAACAGAAATGGCA 425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    361 CGTATCAAAAAGTGGCTGACCTTCTCTCTCGGGCAAACAAGTTGGGACAAGTTCTTCCTG 420

Db    426 CGTATCAAAAAGTGGCTGACCTTCTCTCTCGGGCAAACAAGTTGGGACAAGTTCTTCCTG 485
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480

Db    486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGAGGCCATTCAGAATCTCATCAAGGAG 540

Db    546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGAGGCCATTCAGAATCTCATCAAGGAG 605
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600

Db    606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660

Db    666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCGTCCTCCACCTCCCAT 720

Db    726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCGTCCTCCACCTCCCAT 785
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747

Db    786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812
```

RESULT 4
US-09-949-016-15241
; Sequence 15241, Application US/0994016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15241
; LENGTH: 8093
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15241

Query Match 50.1%; Score 374; DB 4; Length 8093;

```
Qy    554  GCATCACTCTGATGAGGAAGACAGAGAGGCAGTTGTGTGGATCTGACAGGAAATAGACTGACCT  613
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5371  GCATCACTCTGATGAGGAAGACAGAGAGGCAGTTGTGTGGATCTGACAGGAAATAGACTGACCT 5430

Qy    614  ACACAAACTGGAACCAGCGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGC  673
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5431  ACACAAACTGGAACGAGCGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGC 5490

Qy    674  TACTGAAAAATGGCCAGTGAATGACGTCCCCTGCTCCACCTCCACCTCCGGCCGTCTGTG  733
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5491  TACTGAAAAATGGCCAGTGAATGACGTCCCCTGCTCCACCTCCACCTCCGGCCGTCTGTG 5550

Qy    734  AGTTCCCTATCTGA  747
           |||||||||||||
Db   5551  AGTTCCCTATCTGA  5564
```

RESULT 6
US-09-198-603C-25
; Sequence 25, Application US/09198603C
; Patent No. 6337193
; GENERAL INFORMATION:
;   APPLICANT: TULLY, Raymond E.
;   APPLICANT: CALTAGIRONE, G. Thomas
;   APPLICANT: MOYER, Shawn S.
;   APPLICANT: RONNING, Michael T.
;   TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC
;   TITLE OF INVENTION: YEAST
;   FILE REFERENCE: A7290
;   CURRENT APPLICATION NUMBER: US/09/198,603C
;   CURRENT FILING DATE: 1998-11-24
;   NUMBER OF SEQ ID NOS: 26
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 1211
;   TYPE: DNA
;   ORGANISM: Mouse
US-09-198-603C-25

Query Match   27.4%; Score 204.4; DB 3; Length 1211;
Best Local Similarity   71.7%; Pred. No. 1.7e-54;
Matches 268; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

```
Qy    374  GGCTGACCTTCTCTCTCGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAATGGTGAAA  433
           |||  ||||  |||||||||||||||||  ||||||| ||||  |||| ||||||||||||
Db    576  GGGTGCTTCTTCTCTGAGTGAAAAAGTGAAGGCCTTCGTGTCTGGCCACCC  635

Qy    434  TAATGACCTTTGAAAAAGTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTG  493
           |||||| |||||||| |||  ||| ||||| |||||  |||| |||||||||| ||||
Db    636  AGATGAGCCTTGATAGAGTGAAGGCCCCTGTGTCTGCTCCGAATTCCAGGCTCTGTGGCCACTC  695

Qy    494  CCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAAGCCTTCCTGG  553
           |||||||||||||||||||   |||| |||||  ||||| ||||| |||||||||||||
Db    696  CCAGGAATGCTGCAGAGAAACTCGGCCATCCATCCAGAAAGTGGCCAAAGATATTGCCTACTTGG  755

Qy    554  GCATCACTGATGAGGAAGACAGAGAGGCAGTTTGTGATCTGACAGGAAATAGACTGACCT  613
           |||||||  |||| |||| || ||  |||||||| |||||||||||||||  ||||| |
Db    756  GCATCACAGATGTGAGGGTTGAGGCAGTTTTGAGGATCTGACAGGAAAACAGAGTGCGCT  815

Qy    614  ACACAAACTGGAACGAGCGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGC  673
           | ||| ||||||| || | ||||  |  ||||  ||| |||  || | |||||| |||| ||| 
Db    816  ATACTAATTGGAATGATTGGGAGGCCAACACACGGGCGATGGGGAAGACTGTGTGGTGTGA  875

Qy    674  TACTGAAAAATGGCCAGTGAATGACGTCCCCTGCTCCACCTCCACCTCCGGCCGTCTGTG  733
           | |||||||||| |||||| ||||| ||| |||||| | |||  |  |  |  |||| ||
Db    876  TCTTGGGAAATGCCAAGTGGAACGATGTGGAACGATGTCCCCTGCTCTGACTCTTTTTGGCAATATGTG  935

Qy    734  AGTTCCCTATCTGA  747
           | ||| |||| |||
Db    936  AATTCTCTGACTGA  949
```

RESULT 7

US-09-949-016-18336/c
; Sequence 18336, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18336
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-18336

Query Match   25.2%; Score 188; Pred. No. 1.9e-49;
Best Local Similarity   100.0%; Mismatches 0; Indels 0; Gaps 0;
Matches 188; Conservative 0;

```
Qy      1  ATGTCCCTGTTCCATCACTCCCTCTCCTTCTCCGAGTATGGTGGCAGCGTCTTACTCA  60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    597  ATGTCCCTGTTCCATCACTCCCTCTCCTTCTCCGAGTATGGTGGCAGCGTCTTACTCA  538

Qy     61  GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    537  GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT  478

Qy    121  CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    477  CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG  418

Qy    181  GAACCAGG  188
           ||||||||
Db    417  GAACCAGG  410
```

RESULT 8
US-09-949-016-124315/c
; Sequence 124315, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124315
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-124315

Query Match   25.2%; Score 188; DB 4; Length 601;
Best Local Similarity   100.0%; Pred. No. 1.9e-49;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATGTCCCGTTCCATCACTCCCTCCTTCTCCTGAGTGTGGCAGCGTCTTACTCA 60
        |||||||||||||||||||||||||||||||||||| ||||||||
Db 597 ATGTCCCGTGTTCCATCACTCCCTCCTTCTCCTGAGTGTGGCAGCGTCTTACTCA 538

Qy   61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCTCTGAGCTCT 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 537 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGAGCTCT 478

Qy 121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 477 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 418

Qy 181 GAACCAGG 188
        ||||||||
Db 417 GAACCAGG 410

RESULT 9
US-09-198-603C-26
; Sequence 26, Application US/09198603C
; Patent No. 6337193
; GENERAL INFORMATION:
;   APPLICANT: TULLY, Raymond E.
;   APPLICANT: CALTAGIRONE, G. Thomas
;   APPLICANT: MOYER, Shawn S.
;   APPLICANT: RONNING, Michael T.
;   TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC
;   TITLE OF INVENTION: YEAST
;   FILE REFERENCE: A7290.
;   CURRENT APPLICATION NUMBER: US/09/198,603C
;   CURRENT FILING DATE: 1998-11-24
;   NUMBER OF SEQ ID NOS: 26
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
;   LENGTH: 714
;   TYPE: DNA
;   ORGANISM: CHICKEN
US-09-198-603C-26

Query Match   16.9%; Score 126; DB 3; Length 714;
Best Local Similarity 53.0%; Pred. No. 1.2e-29;
Matches 351; Conservative 0; Mismatches 290; Indels 21; Gaps 3;

Qy   79 GATGGCCCAAAAGACCTGCCCTGCCCTGCAGTGATTGCTCTCCAGGCATCAACGGCTTC 138
        ||| ||| | |||||||| |||||||||| |||||
Db   37 GAAGAGAAAAATGTATTCCTGTCCCATCATTCAGTGTAGTGCTCCTGCAGTCAATGGATTA 96

Qy 139 CCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGGGAACCAGGCCAAGGGACTC 198
        ||||||||||||||||| |||||| ||||| ||| ||||| ||||||||||| ||
Db   97 CCAGGCAGAGATGGAAGAGATGTGTCCCAAAGGGGAAAAGGGACCCGGAGAAGGGACTG 156

Qy 199 AGAGGCTTACAGGGCCCCCCCTGGAAAGTTGGGGCCTTCCAGGAAATCCAGGGCCTTCTGGG 258
        ||||| |||||| | |||||| ||| | |||||||| ||| |||
Db 157 AGAGGTCTGCAGGGTTTGCCTGGAAAGCCAGGACCCCAAGGATTAAAAGGAGAGGTGGGA 216

Qy 259 TCACCAGGACCAAAGGGCAAAAGGGAGACCCCTGGAA--------AAAGTCCGGAT 306
        |||||| ||||||| ||||||| |||||||||||||
Db 217 CCACAAGGAGAGAGAAGTCAAAAAGGAGAACGTGGAATTGTTGTAACTGATGACCTCCAC 276

Qy 307 GGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAAACAGAAATGCACGTATC 366
        ||||| | |||| ||| | ||||||
Db 277 CGACAAATAACTGATTTGGAAGCAAAAATCCGGGTATTGGAAGATGACTTAAGCAGATAC 336

Qy 367 AAAAAGTGGCTCAGCCTTCTCCTGGGCAAACAAGTTGGGAACAAGTCTTCCTGACCAAT 426
        ||||| ||| | ||| |||
Db 337 AAAAAGCCTTGAGTTTAAAGGACGTCGTAAACATTGGTAAAAAAATGTTTGTTCTCAACT 396

Qy 427 GGTGAAATAATGACCTTTGAAAAAGTGAAGCCTTGTGTGTCAAGTTCCAGGCCTCGTG 486
        ||| || ||| || || ||| | |||
Db 397 GGAAAGAATATATTATTTTGAAAAGGGAAAAATCCCTTTGTGCAAAAGCTGGAAGTGTGCTT 456

Qy 487 GCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAG-----GAG 540

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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124316
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-124316

Query Match             9.9%;  Score 74;  DB 4;  Length 601;
Best Local Similarity  100.0%;  Pred. No. 4e-13;
Matches   74;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy  115 AGCTCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAA 174
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 AGCTCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAA 542

Qy  175 AAGGGGGAACCAGG 188
        ||||||||||||||
Db  541 AAGGGGGAACCAGG 528
```

RESULT 12
US-09-198-603C-24
```
; Sequence 24, Application US/09198603C
; Patent No. 6337193
; GENERAL INFORMATION:
; APPLICANT: TULLY, Raymond E.
; APPLICANT: CALTAGIRONE, G. Thomas
; APPLICANT: MOYER, Shawn S.
; APPLICANT: RONNING, Michael T.
; TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC
; TITLE OF INVENTION: YEAST
; FILE REFERENCE: A7290
; CURRENT APPLICATION NUMBER: US/09/198,603C
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 1558
; TYPE: DNA
; ORGANISM: RAT
US-09-198-603C-24

Query Match             9.8%;  Score 73.4;  DB 3;  Length 1558;
Best Local Similarity  77.4%;  Pred. No. 1.1e-12;
Matches   89;  Conservative   0;  Mismatches  26;  Indels   0;  Gaps   0;

Qy   185 CAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCTGGAAAGTTGGGGCCTCCAGGAAATC 244
         ||||||||||  ||||||| ||||| ||||||||||||||| |||||||||||||||||
Db  1173 CAGGTCAAGGGCTCAGGGCTTGCAGGGCCCTCAGGGAAACTGGGGCCTCCAGGAAGTG 1232

Qy   245 CAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAGGAGGAGACCCTGGAAAAG 299
         ||||||||||| ||||| | |||||||||||| |||||| || || |||
Db  1233 TAGGAGCCCCTGGAAGTCAAGGACCAAAAGGGGCCAAAAGGGGATCGTGGGAGACAG 1287
```

RESULT 13
US-09-949-016-18342/c
```
; Sequence 18342, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
```

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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18342
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-18342

Query Match             9.6%;  Score 72;  DB 4;  Length 601;
Best Local Similarity  93.8%;  Pred. No. 1.7e-12;
Matches   75;  Conservative   0;  Mismatches   5;  Indels   0;  Gaps   0;

Qy  295 AAAAGTCCGATGGTGATAGTAGCCTGGCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAA 354
        ||  ||  |||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db  129 AATTTCTTAGATGGTGATAGTAGCCTGGCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAA 70

Qy  355 ATGGCACGTATCAAAAAGTG 374
        ||||||||||||||||||||
Db   69 ATGGCACGTATCAAAAAGTG 50
```

RESULT 14
US-09-949-016-124321/c
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; Sequence 124321, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124321
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-124321

Query Match             9.6%;  Score 72;  DB 4;  Length 601;
Best Local Similarity  93.8%;  Pred. No. 1.7e-12;
Matches   75;  Conservative   0;  Mismatches   5;  Indels   0;  Gaps   0;

Qy  295 AAAAGTCCGATGGTGATAGTAGCCTGGCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAA 354
        ||  ||  |||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db  129 AATTTCTTAGATGGTGATAGTAGCCTGGCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAA 70

Qy  355 ATGGCACGTATCAAAAAGTG 374
        ||||||||||||||||||||
Db   69 ATGGCACGTATCAAAAAGTG 50
```

RESULT 15
US-08-365-103B-3
```
; Sequence 3, Application US/08365103B
; Patent No. 5766943
; GENERAL INFORMATION:
; APPLICANT: Lynch, Richard G
; APPLICANT: Nunez, Raphael D.
; APPLICANT: Yodoi, Jungi
; TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
; TITLE OF INVENTION: and Methods of Use for Same
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
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;     ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
;     STREET: 801 Grand Ave. Suite 3200
;     CITY: Des Moines
;     STATE: Iowa
;     COUNTRY: United States
;     ZIP: 50309
; COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/365,103B
;     FILING DATE: 28-DEC-1994
;     CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;     NAME: Nebel, Heidi S.
;     REGISTRATION NUMBER: 37,719
;     REFERENCE/DOCKET NUMBER: Uirf N5-24
; TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (515) 288-3667
;     TELEFAX: (515) 288-1338
; INFORMATION FOR SEQ ID NO: 3:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH: 885 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     FEATURE:
;         NAME/KEY: CDS
;         LOCATION: 24..884
US-08-365-103B-3
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Search completed: June 20, 2005, 17:05:13
Job time : 185 secs

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            GenCore version 5.1.6
    Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   June 20, 2005, 16:02:01 ; Search time 1644 Seconds
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Perfect score: 747
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Scoring table:  IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched:  6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters:  12109378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	747	100.0	747	16	US-10-054-536-2	Sequence 2, Appli
2	747	100.0	747	22	US-10-500-774-2	Sequence 2, Appli
3	747	100.0	3605	9	US-09-880-107-3705	Sequence 3705, Ap
4	747	100.0	3605	16	US-10-054-536-1	Sequence 1, Appli
5	747	100.0	3605	17	US-10-429-160-57	Sequence 57, Appl
6	747	100.0	3605	22	US-10-500-774-1	Sequence 1, Appli
7	741.2	99.2	2159	21	US-10-844-837-99	Sequence 99, Appl

8	684	91.6	684	8	US-09-971-475-2	Sequence 2, Appli
9	444.6	59.5	1409	14	US-10-076-816-54	Sequence 54, Appl
10	373.2	50.0	1069	21	US-10-764-420-2521	Sequence 2521, Ap
11	364.6	48.8	1037	9	US-09-917-800A-1710	Sequence 1710, Ap
12	287.6	38.5	1068	17	US-10-388-934-107	Sequence 107, App
13	222	29.7	419	9	US-09-960-352-11785	Sequence 11785, A
14	186.2	24.9	405	19	US-10-450-472-58	Sequence 58, Appl
15	186	24.9	1802	18	US-10-070-415A-45	Sequence 45, Appl
16	186	24.9	1802	18	US-10-070-415A-49	Sequence 49, Appl
17	186	24.9	1802	18	US-10-070-415A-53	Sequence 53, Appl
18	185.6	24.8	463	19	US-10-469-285-750	Sequence 750, App	c
19	185	24.8	1802	18	US-10-070-415A-41	Sequence 41, Appl
20	185	24.8	1802	18	US-10-070-415A-42	Sequence 42, Appl
21	185	24.8	1802	18	US-10-070-415A-43	Sequence 43, Appl
22	185	24.8	1802	18	US-10-070-415A-44	Sequence 44, Appl
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26	184.4	24.7	1802	18	US-10-070-415A-50	Sequence 50, Appl
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28	184.4	24.7	1802	18	US-10-070-415A-52	Sequence 52, Appl
29	184.4	24.7	1802	18	US-10-070-415A-54	Sequence 54, Appl
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31	184.4	24.7	1802	18	US-10-070-415A-56	Sequence 56, Appl
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33	112.4	15.0	5815	15	US-10-311-455-1208	Sequence 1208, Ap	c
34	108	14.5	542	15	US-10-388-934-108	Sequence 108, App
35	108	14.5	5815	15	US-10-311-455-1207	Sequence 1207, Ap
36	107.2	14.4	240	9	US-09-960-352-14616	Sequence 14616, A
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39	94.6	12.7	1128	13	US-10-830-959-3	Sequence 3, Appli
40	94.6	12.7	1313	14	US-10-116-802-47	Sequence 47, Appl
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42	94.6	12.7	1410	21	US-10-843-641A-5301	Sequence 5301, Ap
43	94.6	12.7	2540	21	US-10-844-837-100	Sequence 100, App
44	93.6	12.5	408	19	US-10-450-472-60	Sequence 60, Appl
45	92.6	12.4	534	20	US-10-830-959-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-054-536-2
; Sequence 2, Application US/10054536
; Publication No. US2003016224BA1
; GENERAL INFORMATION:
; APPLICANT: Wakamiya, No. US20030162248Alutaka
; TITLE OF INVENTION: RECOMBINANT HUMAN MANNAN-BINDING PROTEINS AND PROCESS
; TITLE OF INVENTION: FOR PRODUCING THE SAME
; FILE REFERENCE: 19036/36614
; CURRENT APPLICATION NUMBER: US/10/054,536
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/JP98/03311
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 10-11864
; PRIOR FILING DATE: 1998-01-23
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-054-536-2

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Best Local Similarity 100.0%; Pred. No. 2.9e-234;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; LENGTH: 3605
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accesion No. US2002014291A1 X15422
US-09-880-107-3705

Query Match   100.0%;   Score 747;   DB 9;   Length 3605;
Best Local Similarity   100.0%;   Pred. No. 6e-234;
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Db    366 CCGGATGGTGATAGTAGCCTGCCTCAGAAAGAAAAGCTTCGAAACAGAAATGGCA 425

Qy    361 CGTATCAAAAAGTGGCTGACCTTCTCTCGGGCAAACAAGTTCTTCCTG 420
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Db    426 CGTATCAAAAAGTGGCTGACCTTCTCTCGGGCAAACAAGTTCTTCCTG 485

Qy    421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
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Db    486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy    481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
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Db    546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy    541 GAAGCCTTCCTGGGCATCACAAACTGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 600
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Qy    601 AATAGACTGACCTACACAAACTGAAAATGGCTCGTTCACCTCCAT 660
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Qy    661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGAATGACGTCCCCTGCTCCACCTCCCAT 720
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RESULT 4
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; Sequence 1, Application US/10054536
; Publication No. US2003016224BA1
; GENERAL INFORMATION:
; APPLICANT: Wakamiya, No. US20030162248Alutaka
; TITLE OF INVENTION: RECOMBINANT HUMAN MANNAN-BINDING PROTEINS AND PROCESS
; TITLE OF INVENTION: FOR PRODUCING THE SAME
; FILE REFERENCE: 19036/36614

;
; CURRENT APPLICATION NUMBER: US/10/054,536
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/JP98/03311
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 10-11864
; PRIOR FILING DATE: 1998-01-23
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
; LENGTH: 3605
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(809)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (126)..(809)
US-10-054-536-1

Query Match   100.0%;   Score 747;   DB 16;   Length 3605;
Best Local Similarity   100.0%;   Pred. No. 6e-234;
Matches   747;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy      1 ATGTCCCGTTCCATCACTCCCTCCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 ATGTCCCGTTCCATCACTCCCTCCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy     61 GAAACTGTGACCTGTGAGGATGCCCAGTGATTGCCTGTAGCTCT 120
            |||||||||||||||||||||||||||||||||||||||||||
Db    126 GAAACTGTGACCTGTGAGGATGCCCAGTGATTGCCTGTAGCTCT 185

Qy    121 CCAGGCATCAACGGCTTCCAGGCAAAGATGGCGTGATGGCCACCAAGGGAGAAAAGGGG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 CCAGGCATCAACGGCTTCCAGGCAAAGATGGCGTGATGGCCACCAAGGGAGAAAAGGGG 245

Qy    181 GAACCAGGCCAAGGGCTTACAGGGCCTCAGAGGCTTACAGGGCCTCCAGGA 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 GAACCAGGCCAAGGGCTTACAGGGCCTCAGAGGCTTACAGGGCCTCCAGGA 305

Qy    241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGGCCAAAAGGGCCAAAAGGAGACCCTGAAAAAGT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGGCCAAAAGGGCCAAAAGGAGACCCTGAAAAAGT 365

Qy    301 CCGGATGGTGATAGTAGCCTGGCTGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 CCGGATGGTGATAGTAGCCTGGCTGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425

Qy    361 CGTATCAAAAAGTGGCTGACCTTCTCTCGGGGAACAAGTTCTTCCTG 420
            |||||||||||||||||||||||||||||||||||||||||||||||
Db    426 CGTATCAAAAAGTGGCTGACCTTCTCTCGGGGAACAAGTTCTTCCTG 485

Qy    421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTCTGTGTCAAGTTCCAGGCC 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTCTGTGTCAAGTTCCAGGCC 545

Qy    481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAAGACAAGGGCAGTTGTGTGATCTGACAGGA 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAAGACAAGGGCAGTTGTGTGATCTGACAGGA 605

Qy    541 GAAGCCTTCCTGGGCATCACACAAACTGGAACCCAACAAATGCTGAACCCAACAATGCTGGTCTGATGAA 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 GAAGCCTTCCTGGGCATCACACAAACTGGAACCCAACAAATGCTGAACCCAACAATGCTGGTCTGATGAA 665

Qy    601 AATAGACTGACCTACACAACTGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    666 AATAGACTGACCTACACAACTGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy    661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGAATGACGTCCCCGTCCCCTGCTCCACCTCCCAT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGAATGACGTCCCCGTCCCCTGCTCCACCTCCCAT 785

Qy    721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
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Db    786 CTGGCCGTCGTGTGAGTTCCCTATCTGA 812
          ||||||||||||||||||||||||||||

RESULT 5
US-10-429-160-57
; Sequence 57, Application US/10429160
; Publication No. US2004002376A1
; GENERAL INFORMATION:
;   APPLICANT: Ward, Teresa R
;   APPLICANT: Mao, Mao
;   APPLICANT: Linsley, Peter S
;   APPLICANT: Lund, Lund
;   TITLE OF INVENTION: LXR Ligand Induced Genes and Proteins
;   FILE REFERENCE: RS0200
;   CURRENT APPLICATION NUMBER: US/10/429,160
;   CURRENT FILING DATE: 2003-05-02
;   PRIOR APPLICATION NUMBER: US 60/377,714
;   PRIOR FILING DATE: 2002-05-03
;   SOFTWARE: PatentIn version 3.1
;   NUMBER OF SEQ ID NOS: 111
; SEQ ID NO 57
;   LENGTH: 3605
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-429-160-57

Query Match          100.0%;    Score 747;   DB 17;  Length 3605;
Best Local Similarity 100.0%;   Pred. No. 6e-234;
Matches   747;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 ATGTCCCTGTTTCCATCACTCCCCTCCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    66 ATGTCCCTGTTTCCATCACTCCCCTCCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy    61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCCCTGCCGTGAGTGCTGTAGCTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCCGTGATGGCACCAAGGGAGAAAAGGGG 185

Qy   121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy   181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAAAGT 305

Qy   241 AATCCAGGGCCTTCGGGTCACCGGACCAGGACCAAAGGAGACCCCTGGAAAAAGT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 AATCCAGGGCCTTCGGGTCACCGGACCAGGACCAAAGGAGACCCCTGGAAAAAGT 365

Qy   301 CCGGATGGTGATAGTAGCCTGCCTCTCTCTGGGAACCAAGTTCTTCCTG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366 CCGGATGGTGATAGTAGCCTGCCTCTCTCTGGGAACCAAGTTCTTCCTG 425

Qy   361 CGTATCAAAAAGTGGCTGACCTTTCTCTCTGGGAACCAAGTTCTTCCTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426 CGTATCAAAAAGTGGCTGACCTTTCTCTCTGGGAACCAAGTTCTTCCTG 485

Qy   421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTGCAAGGCC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTGCAAGTTCCAGGCC 545

Qy   481 TCTGTGGCCACCCCAGGAATGCTGCAGAGAATGCGAGCCATTCAGAATCTCATCAAGGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   546 TCTGTGGCCACCCCAGGAATGCTGCAGAGAATGCGAGCCATTCAGAATCTCATCAAGGAG 605

Qy   541 GAAGCCTTCCTGGGCATCACTGATGAGACAGAGGGCAGTTTGTGGATCTGACAGGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   606 GAAGCCTTCCTGGGCATCACTGATGAGACAGAGGGCAGTTTGTGGATCTGACAGGA 665

Qy   601 AATAGACTGACCTACACAAACTGAACCAGAGGGTGAACCAACAATGTGGTTCTGATGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   666 AATAGACTGACCTACACAAACTGAACCAGAGGGTGAACCAACAATGTGGTTCTGCCACCTCCAT 725
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GATTGTGATTGCTACTGAAAAATGGCCAGTGAATGACGTCCCGTCCCCTGTCCACCTCCAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   726 GATTGTGATTGCTACTGAAAAATGGCCAGTGAATGACGTCCCGTCCCCTGTCCACCTCCAT 785

Qy   721 CTGGCCGTCGTGTGAGTTCCCTATCTGA 747
          ||||||||||||||||||||||||||||
Db   786 CTGGCCGTCGTGTGAGTTCCCTATCTGA 812

RESULT 6
US-10-500-774-1
; Sequence 1, Application US/10500774
; Publication No. US2005012389A1
; GENERAL INFORMATION:
;   APPLICANT: FUSO PHARMACEUTICAL INDUSTRIES, LTD.
;   TITLE OF INVENTION: Anti-HIV Agent
;   FILE REFERENCE: 03P451WO
;   CURRENT APPLICATION NUMBER: US/10/500,774
;   CURRENT FILING DATE: 2004-07-06
;   PRIOR APPLICATION NUMBER: JP 2002-189534
;   PRIOR FILING DATE: 2002-06-28
;   NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 1
;   LENGTH: 3605
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-500-774-1

Query Match          100.0%;    Score 747;   DB 22;  Length 3605;
Best Local Similarity 100.0%;   Pred. No. 6e-234;
Matches   747;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 ATGTCCCTGTTTCATCACTCCCCTCCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    66 ATGTCCCTGTTTCATCACTCCCCTCCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy    61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCCGTGAGTGCTGTAGCTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCCGTGAGTGCTGTAGCTCT 185

Qy   121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy   181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy   241 AATCCAGGGCCTTCTGGGTCACCAGGACCAGGACCAAAGGGCCAAAAGGAGACCCTGGAAAAAGT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 AATCCAGGGCCTTCTGGGTCACCAGGACCAGGACCAAAGGGCCAAAAGGAGACCCTGGAAAAAGT 365

Qy   301 CCGGATGGTGATAGTAGCCTGCCTGCCTCAGAGAAGAAAGCTCGCAAACAGAAATGGCA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366 CCGGATGGTGATAGTAGCCTGCCTGCCTCAGAGAAGAAAGCTCGCAAACAGAAATGGCA 425

Qy   361 CGTATCAAAAAGTGGCTGACCTTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426 CGTATCAAAAAGTGGCTGACCTTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy   421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTGTCAAGTTCCAGCC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTGTCAAGTTCCAGCC 545

Qy   481 TCTGTGGCCACCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   546 TCTGTGGCCACCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy   541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAGGGCAGTTTGTGGATCTGACAGGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAGGGCAGTTTGTGGATCTGACAGGA 665
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Qy  541  GAAGCCTTCCTGGGTCATCACTGATGAGAGAGAGACAGAAGGGCAGTTGTGTGGATCGACACAGGA  600
         ||||||||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db 1219  GAAGCCTTCCTGGGTATCACTGATGAGAGAGAGACAGAAGGGCAGTTGTGTGGATCGACACAGGA  1278

Qy  601  AATAGACTGACCTACACAAACTGAACGAGGGTGAACCCAACAATGCTCGTTCTGATGAA  660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1279  AATAGACTGACCTACACAAACTGAACGAGGGTGAACCCAACAATGCTCGTTCTGATGAA  1338

Qy  661  GATTGTGTATTGCTACTGAAAAATGGCCAGTGAAATGGCAAATGGCTCCCACCTCCAT  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1339  GATTGTGTATTGCTACTGAAAAATGGCCAGTGAATGACGTCCCCGCTCCACCTCCCAT  1398

Qy  721  CTGGCCGTCTGTGAGTTCCCTATCTG  746
         |||||||||||||||||||||||||
Db 1399  CTGGCCGTCTGTGAGTTCCCTATCGG  1424


RESULT 8
US-09-971-475-2
; Sequence 2, Application US/09971475
; Publication No. US2002086817A1
; GENERAL INFORMATION:
;  APPLICANT: Kawasaki, Toshisuke
;  TITLE OF INVENTION: Anticancer agent
;  FILE REFERENCE: ADT 308
;  CURRENT APPLICATION NUMBER: US/09/971,475
;  CURRENT FILING DATE: 2001-10-04
;  PRIOR APPLICATION NUMBER: US 09/468,705
;  PRIOR FILING DATE: 1999-12-21
;  PRIOR APPLICATION NUMBER: PCT/JP98/03697
;  PRIOR FILING DATE: 1998-08-19
;  PRIOR APPLICATION NUMBER: JP 239113/97
;  PRIOR FILING DATE: 1997-08-21
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;  LENGTH: 684
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-971-475-2

Query Match            91.6%;  Score 684;  DB 9;  Length 684;
Best Local Similarity  100.0%;  Pred. No. 1.4e-213;
Matches  684;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   61  GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTCCCGTGATTGCCCTGAGCTCT  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTCCCGTGATTGCCCTGAGCTCT   60

Qy  121  CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG  120

Qy  181  GAACCAGGCCAAGGGCTTACAGGGCTTACAGGGCCTCCAGGA  240
         ||||||||||||||||||||||||||||||||||||||||||
Db  121  GAACCAGGCCAAGGGCTTACAGGGCTTACAGGGCCTCCAGGA  180

Qy  241  AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGAAAAGT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGAAAAGT  240

Qy  301  CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAACAGAATGGCA  360
         |||||||||||||||||||||||||||||||||||||||||||
Db  241  CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAACAGAATGGCA  300

Qy  361  CGTATCAAAAGTGGCTGACCTTGGGGAACAAGTTCTTCCTG  420
         |||||||||||||||||||||||||||||||||||||||||
Db  301  CGTATCAAAAGTGGCTGACCTTGGGGAACAAGTTCTTCCTG  360

Qy  421  ACCAATGGTGAAATAATGACCTTTGAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGCC  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  ACCAATGGTGAAATAATGACCTTTGAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGCC  420
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Qy  601  AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTCGGTTCTGATGAA  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  666  AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTCGGTTCTGATGAA  725

Qy  661  CTGGCCGTCTGTGAGTTCCCTATCTGA  747
         |||||||||||||||||||||||||||
Db  726  GATTGTGTATTGCTACTGAAAAATGGCCAGTGAAATGGCAAATGGCTCCCACCTCCCAT  785

Qy  721  CTGGCCGTCTGTGAGTTCCCTATCTGA  747
         |||||||||||||||||||||||||||
Db  786  CTGGCCGTCTGTGAGTTCCCTATCTGA  812


RESULT 7
US-10-844-837-99
; Sequence 99, Application US/10844837
; Publication No. US2005014932A1
; GENERAL INFORMATION:
;  APPLICANT: Imboden, Michael
;  APPLICANT: Homan, Jane
;  APPLICANT: Bremel, Robert D.
;  TITLE OF INVENTION: Targeted Biocides
;  FILE REFERENCE: IOGEN-09014
;  CURRENT APPLICATION NUMBER: US/10/844,837
;  CURRENT FILING DATE: 2004-05-13
;  NUMBER OF SEQ ID NOS: 101
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 99
;  LENGTH: 2159
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-844-837-99

Query Match            99.2%;  Score 741.2;  DB 21;  Length 2159;
Best Local Similarity  99.6%;  Pred. No. 3.8e-232;
Matches  743;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy    1  ATGTCCCGTGTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  679  ATGTCCCGTGTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA  738

Qy   61  GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTCCCGTGAGTGCCTGTAGCTCT  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  739  GAAACTGTGGCCTGTGAGGATGCCCAAAAGACCTGCCCTCCCGTGAGTGCCTGTAGCTCT  798

Qy  121  CCAGGCATCAACGGCTTCCCAGGCCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  799  CCAGGCATCAACGGCTTCCCAGGCCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG  858

Qy  181  GAACCAGGCCAAGGGCTTACAGGGCTTACAGGGACCAAAAGT  240
         ||||||||||||||||||||||||||||||||||||||||||
Db  859  GAACCAGGCCAAGGGCTTACAGGGCTTACAGGGACCAAAAGT  918

Qy  241  AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGAAAGCTCTGCAAACAGAAATGGCA  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  919  AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGAAAGCTCTGCAAACAGAAATGGCA  978

Qy  301  CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAGAGAAAGCTCTGCAAACAGAAATGGCA  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  979  CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAGAGAAAGCTCTGCAAACAGAAATGGCA 1038

Qy  361  CGTATCAAAAGTGGCTGACCTTGGGCAAACAAGTTGGGAACAGTTCTTCCTG  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1039  CGTATCAAAAGTGGCTGACCTTGGGCAAACAAGTTGGGAACAGTTCTTCCTG 1098

Qy  421  ACCAATGGTGAAATAATGACCTTTGAAAAGTGAAGGCCATTCAGAATCTCATCAAGGAG  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1099  ACCAATGGTGAAATAATGACCTTTGAAAAGTGAAGGCCATTCAGAATCTCATCAAGGAG 1158

Qy  481  TCTGTGCGCACCCCCAGGAATGCTGAGAATGCTGAGAATCTCATCAAGGAG  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1159  TCTGTGCGCACCCCCAGGAATGCTGAGAATGCTGAGAATCTCATCAAGGAG 1218
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Qy  295  AAAGTTCCGGATGGTGATGTAGTAGCCTGGCTGCCTCAGAGAATAAAGTCTCTGCAAACAGAA  354
              ||||| ||||||||||        |||||||||| |||||| ||||| ||| ||||||||
Db  313  GAAAATATGGGTGACTATATTCCGCTGGCTACTTCAGAAGAGCAACTCTACAATCTGAA  372

Qy  355  ATGGCACGTATCAAAAAGTGGCTGCAGAGGACAGAAGGGCAGTTTGTGATCTGGAACAAGTC  414
              |||| ||||||||||| |||||  |    |||||| ||| ||||||| |||||
Db  373  TTGAACCAGATCAAAAACTGGCTAATCTTCTCTCTGGGCAAAAGAGTGGGAAGAAGGCA  432

Qy  415  TTCCTGACCAATGGTGAAATAATGACCTTGAAAAAGTGAAGGCCTTCTGTGTGTCAAGTTC  474
              |||| |||||||| |||| ||||||| ||||  ||||||| |  ||||||| ||||||
Db  433  TTTTTTACCAATGGTAAAAAGATGCCTTTTAATGAAGTGAAGACTCTGTGCACAGTTC  492

Qy  475  CAGGCCTCTGTGGCCACCCCAGGAATGCTGCAGAATGGAGCCATTCAGAATCTCATC  534
              |||| ||||| |||||||||| ||||||||  || ||||||||||| |||| ||||
Db  493  CAGGGCCGTGTGGGCCACCCCATGAATGCTGAAGAAACACAGGGCCCTCAAGGATTTAGTC  552

Qy  535  AAGGAGGAAGCCTTCCTGGCATCATGATGAGAAGACAGAAGGGCAGTTTGTGGATCTG  594
              ||   ||||||||||||| |||||| |||  |||||| |||| ||| |||||||||||
Db  553  ACTGAAGAGAGGCCTTCCTGGGCATCACAGATCAGGAGACTGAAGGGCAAATTTGTGGATCTGA  612

Qy  595  ACAGGAAATAGACTGACCTACACAAACTGGAACACTGGTAGCAGAGGGTGAACCAACAATGCTTGGTTCT  654
              ||||||||  | ||||||| |||||||||||  |   | ||||||| || |||| ||||||||||
Db  613  ACAGGAAAGGGGGGTGACCTACCAACAAACTGGAATGATGGGCAGCGAATGATGGGCAGCCAGAACAGACTTGTTCCGCC  672

Qy  655  GATGAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTGCCCCTGCTCCACC  714
              | ||||| |||||| | || ||||||  |||||| || ||||| |     ||| |||||
Db  673  GGGGAGCACTGTGTGACACTTCTGTCGGACGGCACATGCGCTTGTTCCGCC  732

Qy  715  TCCCATCTGCCGTCTGTGAGTTCCCTATCTGA  747
              ||| || |||||||||||| ||  | |||||
Db  733  TCCTTTTTGACCGTCTGTGAATTCTCTCTGA  765
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RESULT 10
US-10-764-420-2521
; Sequence 2521, Application US/10764420
; Publication No. US2005008487421
; GENERAL INFORMATION:
; APPLICANT: Lum, Pek Yee
; APPLICANT: Tan, Yejun
; APPLICANT: Dai, Hongyue
; TITLE OF INVENTION: Methods For Determining Whether An Agent
; TITLE OF INVENTION: Possesses A Defined Biological Activity
; FILE REFERENCE: ROSA122057
; CURRENT APPLICATION NUMBER: US/10/764,420
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,797
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/474,413
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 3683
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2521
; LENGTH: 1069
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-764-420-2521

Query Match   50.0%;   Score 373.2; DB 21; Length 1069;
Best Local Similarity 71.7%;   Pred. No. 2e-111;
Matches   518; Conservative   0; Mismatches 198; Indels   6; Gaps   2;

```
Qy   26  TCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCAGAAACTGTGACCTGTGAGGATGCCC   85
             ||||| ||  |||  | || |  ||    ||| |||||| | | |||||||| |
Db  196  TCCTTCTGTGTGTGTCGGTGCAGTGGTTATGCAGAGACCTTTATGCAGAGACCTTAACC---GAAGGTGTC  252

Qy   86  AAAAGACCTGCCCTGACAGTGATTGCCTGTAGCTTCTCCAGGCATCAACGGCTTCCCAGGCA  145
             |||| ||| | ||   |||| |||||||| ||  |  ||||| ||  |||| || ||||
Db  253  AAAAATTCCTGCCCT---GTGGTTACCTACCTGCAGTTCTCCAGGCCTGAATGCGTCTCCAGGCCA  309

Qy  146  AAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGGGAACCAGGCCAAGGGCTTCAGAGGCT  205
             ||||||| ||||||| |  ||||||||||||| || ||||||||  || |  ||| || |
```

RESULT 9
US-10-076-816-54
; Sequence 54, Application US/10076816
; Publication No. US20030056244A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Ning
; APPLICANT: Rodrguez, Raymond
; APPLICANT: Hagie, Frank E.
; TITLE OF INVENTION: Feed Additive Compositions and Methods
; FILE REFERENCE: 50665-8021.US00
; CURRENT APPLICATION NUMBER: US/10/076,816
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/269,188
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/847,232
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/266,929
; PRIOR APPLICATION NUMBER: US 60/201,182
; PRIOR FILING DATE: 2001-02-06
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 1409
; TYPE: DNA
; ORGANISM: Bos taurus
US-10-076-816-54

Query Match   59.5%;   Score 444.6; DB 14; Length 1409;
Best Local Similarity 76.4%;   Pred. No. 8.1e-135;
Matches   575; Conservative   0; Mismatches 169; Indels   9; Gaps   2;

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Qy    1  ATGTCCCTGTTTCCATCACTCCCTCCTCTCCTCTCCTGAGTATGGTGGCAGCGTCTT-----   55
             ||||| |||||| ||||||| |||  || | ||| ||||| | ||||| ||| ||
Db   16  ATGTCGCTGTTTACATCACTTCCTTTCTTTTCTTCCTGACTGCGGTGCGACGCATCCTTGTGCA   75

Qy   56  -ACTTCAGAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGACAGTGATTGCCTGT  114
              |||| |||| |||||||| | ||| |||||  || |||| |||||  ||| |||||||||
Db   76  GACACAGAAACAGAGAACTGTGACAGCGCTTCCCAGGCGCATCCAGC---CCGTGATTGCCTGTGCAGCA  132

Qy  115  AGCTTCTCCAGGCATCAACGGCTTCCCAGGCAAGATGGGCGTGATGGCCACCAAGGGAGAA  174
             ||||| |||||||||||| | | |||||||||| |||||| ||||||||| ||||||||||
Db  133  GGTCCTCCGGGCATCAATGCAGTCCCAGGCAAAGATGGGCCGTGATGGCCGCCAAGGGAGAA  192

Qy  175  AAGGGGGAACCAGGCCAAGGGCTTCAGAGGCTTACAGGGCCCCTGGGAAAGTTGGGGCCT  234
             ||| | |||||||||||| | || ||||||||  ||||| |||  ||| |||| |||| |
Db  193  AAGGGAGAACCAGGCCAGGTCAAGGACTCAGAGGCTCGCAGGCGCCCCGGGGCCAAAAAAGGG  252

Qy  235  CCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAGGACCCAAAAGGGCCAAAAAGGAGACCCTGGA  294
             ||||||||| |||| ||| ||||| ||||||| |||||| | |  |||||  ||||||||||||||
Db  253  AAAAATTCCTGCCCT--GTGGTTACCTACCTGCAGTTCTCCAGGCCTGAATGCGTCTCCAGGCCTCAGAGGCT  312
```

```
Qy  481  TCTGTGGGCCACCCCAGGAGAATGCTGCAGAGAATGGAGCCATTCATCAAGGAG  540
             |||||||||||||||||||||||||||||||||||||||||||||||
Db  421  TCTGTGGGCCACCCCAGGAGAATGCTGCAGAGAATGGAGCCATTCATCAAGGAG  480

Qy  541  GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGATCTGACAGGA  600
             |||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  481  GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGATCTGACAGGA  540

Qy  601  AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCAACAATGCTGGTTCTGATGAA  660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCAACAATGCTGGTTCTGATGAA  600

Qy  661  GATTGTGTATTGCTACTGAAAAATGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  GATTGTGTATTGCTACTGAAAAATGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT  660

Qy  721  CTGGCCGTCTGTGAGTTCCCTATC  744
             ||||||||||||||||||||||||
Db  661  CTGGCCGTCTGTGAGTTCCCTATC  684
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; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
  NUMBER OF SEQ ID NOS: 1740
  SOFTWARE: PatentIn Ver. 2.1
  SEQ ID NO 1710
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US2002019462A1 NM_022704
  US-09-917-800A-1710

  Query Match  48.8%;  Score 364.6;  DB 9;  Length 1037;
  Best Local Similarity  70.7%;  Pred. No. 1.3e-108;
  Matches 483;  Conservative 0;  Mismatches 200;  Indels 0;  Gaps 0;
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```
Qy   65 CTGTGACCTGTGAGGATGCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGTCTCCAG 124
            ||||||  ||   ||  |  ||||||||| ||  ||| ||| ||||||| |||||||  |
Db  233 CCGAGACCTTAACCAAGGGGCTCAAAGTAGCTGCCCTGTGATTGCCTGCCAGTTCTCCGG 292

Qy  125 GCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAAGGGGGAAC 184
Db  293 CCTGGAACGGCTTCCCAGGCAAAGATGGGCAAAGATGGGCCAAGGGAGAAAAAGGGAGAAC 352

Qy  185 CAGGCCAAGGGCTTCAGAGGCTTACAGGGGCCCCCCTGGAAAGTTGGGCGTCCAGGAAATC 244
Db  353 CGGGTCAAGGCCTCAGAGGCTTGCGAGGGCCTCCTGGAAAAGTAGGACCTGCAGGGCCCC 412

Qy  245 CAGGGCCTTCTGGTCACCAGGACCAAAGGCCAAAACGAGACCCTGGAAAAAGTCCGG 304
Db  413 CAGGGAAATCCTGGGTCAAAAGGACTGGGTCAAAAGGACCAACGGAGAGAGTGTAG 472

Qy  305 ATGGTGATAGTAGCCTGGCTGCTCCAGAAACAGAAGAAGCTCGCAAACAGAAATGCCACGTA 364
Db  473 AATTTGATACTACCAACATTGATTTAGAAATTGCAGCCCTGCGATCGGAGCTGAGAGCTA 532

Qy  365 TCAAAAGTGGCTGACCTTCTCTCTCTGGGCAAACAAGTTCTTCCTGACCA 424
Db  533 TGAGAAGTGGGGTGCTCCTTTCTCATGAGTGAAAATGTTGGAAAGAAGTACTTCATGAGCA 592

Qy  425 ATGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCGACTG 484
Db  593 GTGTTAGAAGGATGCCCCTTAACAGAGGCGAAGGCTCTGTGCTCCGAACTCCAGGGCACTG 652

Qy  485 TGGCCACCCCAGGAATGCTGCAGAGATGCTGAGCCATTCAGAATCTCATCAAGGAGGAAG 544
Db  653 TGGCCACTCCCAGGAATGCTGAGGAGATAGGGCCATCCAGAATGTGGCCAAAGATGTTG 712

Qy  545 CCTTCCTGGCATCACTGATGAGAAGACAGAAGGGCAGTTGTCGATCGACAGGAAATA 604
Db  713 CCTTCTTGGGCATAAGCGACCAGAGGACTGAAAACGTTTTGAGGACCTGACAGGAAACA 772

Qy  605 GACTGACCTGGCTAGCAACTGGGCTGTGAACCCAGAGGTGAGCCTGGTTCTGATGAAGATT 664
Db  773 GAGTGCGCTCACACTAACTGGAATGAGGGTGAGCCCAACAATGTGGGCTTCTGGGGAAAACT 832

Qy  665 GTGTATTGCTACTGAAAAATGGCCAGTGAATGACGTCCCCTGCTCCACCTCTGG 724
Db  833 GTGTGGGTGCTCTTGACAAATGGAAGTGGAAGTGGCAATGGAATGACGTTCCTTGCTCCTTTTTGG 892

Qy  725 CCGTCTGTGAGTTCCCTATCTGA 747
Db  893 TAGTTTGTGAATTCTCTGACTGA 915
```

```
Db  310 AAGATGGACGTGACGGTGCCAAGGGAGAAAAAGGGAGGAGAACCAGTGCAGGGCTCAGAGGCT 369
Qy  206 TACAGGGCCCCCCTGGAAAGTTGGGCGTTCGGGCCTTCGGGTCACCAG 265
Db  370 TGCAAGGCCCTCCTGGAAAAGTAGGAGACCTACAGGACCCCAGGGAATCCGGGGTTAAAAG 429

Qy  266 GACCAAAGGGCAAAAAGGAGGAGACCCTGAAAAAAGTCCGGATCGTGATAGTAGCCTGGCTG 325
Db  430 GAGCAGTTGGGACCGAAGGAGACCCGTGGGGACAGAGCAGAATTTGATACTAGCGAAATTG 489

Qy  326 CCTCAGAAAGAAAGCTCTGCAAACAGAAATGGCACGTGATCAAAAAGTGGCTGACCTTCT 385
Db  490 ATTCAGAAATTGCAGCCCTACGATCAGAGCTGAGAGCCCTGAGAAACTGGGTGCTCTTCT 549

Qy  386 CTCTGGGCAAACAAGTTGGACAGTTCTTCCTGACCAAATGTGAAATAATGACCTTTG 445
Db  550 CTCTGAGTGAAAAATGTTGGAAAGAAGTATTTTGTGAGCAGTGTTAAAAAGATGAGCCTTG 609

Qy  446 AAAAAGTGAAGGCCTTGTGTGTCGACCTGCCTGTGGCCACCCCCAGGAATGCTG 505
Db  610 ACAGAGTGAAGGCCCTGTGTCTCCGAATTCCAGGGCTCTGTGCTCCTCCAGGAATGCTG 669

Qy  506 CAGAGAATGGAGCCATCCAGAATCTCATCAAGGAGGAAGCCTTCCTGGGCATCACTGATG 565
Db  670 AGGAAAACTCCGGCCATCCAGAAGTGCCCAAAGATATTGCCTACTTGGGCATCACACAGATG 729

Qy  566 AGAAGACAGAAGGGCAGTTGTCGATCGACAGGAAATAGACTGACCTACACAAACTGGA 625
Db  730 TGAGGGGTTGAGGCAGTTTGAGGATCTGACCAGGAAAACAGAGCGCGTATACTAATTGGA 789

Qy  626 ACGAGGGTGACCCAACAATGCTGGTTCTGATGAAGAATGTGTATTGCTACTGAAAAATG 685
Db  790 ATGATGGGAGCGCCCAACAACACGCGGCGAAGACTGTGTGTGATCTTGGTGATCTTGGGAAATG 849

Qy  686 GCCAGTGGAATGCAGCTGCACGTCCCCTGCTCCACCTCCACTTGCCGTGGTTCCCTATCT 745
Db  850 GCAAGTGGAACGATGTCCCCTGCTCTGACTCTGTTTTTGGCAATCTGTGAATTCTCTGACT 909

Qy  746 GA 747
Db  910 GA 911
```

```
RESULT 11
US-09-917-800A-1710
; Sequence 1710, Application US/09917800A
; Patent No. US2002019462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884

RESULT 12
US-10-388-934-107
; Sequence 107, Application US/10388934
; Publication No. US2004005547A1
; GENERAL INFORMATION:
; APPLICANT: Boess, Franziska
; APPLICANT: Suter-Dick, Laura
```

; APPLICANT: Wolf, Detlef
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
; FILE REFERENCE: 21199
; CURRENT APPLICATION NUMBER: US/10/388,934
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 02005336.9
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 02015657.6
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 862
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-388-934-107

Query Match   38.5%;   Score 287.6; DB 17; Length 1068;
Best Local Similarity   68.1%;   Pred. No. 2.6e-83;
Matches 417; Conservative   0; Mismatches 189; Indels   6; Gaps   1;

Qy   142 GGCAAGAGATGGGCGTGATGGCACCAGGGAGAAAAGGGGAACCAGGCCAAGGGCTCAGA 201
           |||| ||||| ||| |||||| |||||| || ||||||||| |||||||||||||
Db   64 GGCAGAGACGGGAGGATGGGCCCAAAGGGGAGAGGGAGAACCAGGTCAAGGGCTCAGG 123

Qy   202 GGCTTACAGGGCCCCCTGGAAAGTTGGGGCCTCCAGGAAATCCAGGGCCTTCGTGGTCA 261
           ||||| |||||||| ||||||| || ||||||||||||| ||||||||| ||||||||
Db   124 GGCTTGCAGGGCCCTCCAGGGAAACTTGGGGCCTCCAGGAGTGTAGGAGCCCCTGGAAGT 183

Qy   262 CCAGGACCAAAGGGCCAAAAAGGAGGACCCTGGAAAAAAGTCCGGATGGTGATAGTAGCCTG 321
           ||||||||||| |||||||||| || ||||| ||| ||| || | | ||| ||||||
Db   184 CAAGGACCAAAAGGCCAAAAAGGGGATCGTGGAGACAGCAGCCATTGAGGTGAAGCTG 243

Qy   322 GC------TGCCTCAGAAGAAAAGTCTGCAAACAGAAAGTCGACGTATCAAAAAAGTGG 375
           || ||||| ||| ||||||| ||||| | |||||| ||| ||||| ||| |||
Db   244 GCAAATATGGGAGGCAGAGATAAACACCCTGAAGTCAAAACTGGAGCTAACCAACAAGTTG 303

Qy   376 CTGACCTTCTTCTGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAATGGTGAAATA 435
           ||||||||| | |||| ||||||| ||||||||||| || ||||| |||||||||
Db   304 CATGCCTTCTCCATGGGTAAAAGTCTGGGAAGAAGTTCTTTGTGACCAACCATGAAAGG 363

Qy   436 ATGACCTTTGAAAAAGTGAAGGCCTTCGTGTCAAGTTCCACCCCCC 495
           |||| || || |||||||| || ||||||| ||||||||||| |||||
Db   364 ATGCCCTTTCCAAAGTCAAGGCCCTGTGTCTCAGAGCCACTGTGGCTATCCCC 423

Qy   496 AGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAGAGCCTTCCTGGGC 555
           |||||||||| ||||| |||||||| ||| | || ||| ||||||| ||| ||||| |||
Db   424 AGGAATGCTGACGAGAACAAGGCCATCCAGAAGTCCTAAAACCTCTGCCCTCCTAGGC 483

Qy   556 ATCACTGATGAGAAGAACAGAGAGGGCAGTTTGTTGGATCTGACACAGGAAATAGACTGACCTAC 615
           |||| |||| || || | |||| || || || ||| ||||| ||||| || ||||||| |||
Db   484 ATCACGGACGAGTGACTGAAGCCAATTCATGTATGTGACAGGGGGGGAGGCTCACCTAC 543

Qy   616 ACAAACTTGGAACCAGCAGGGTGAACCAACCAACAATGCTGGTTCTGATGAAGATTGTGTATTGCTA 675
           || | |||||| || |||| ||||||| | || |||||| ||||||||||| ||||||| |||
Db   544 AGCAACTGGAAAAAGGATGAGCCCAATGACCATGGCTTCTCGGGGAAGACTGTGTCACTATA 603

Qy   676 CTGAAAAATGGCCAGTGAACAGTGAATGAGCGTCCCCTGCCTCCCACCTCCCATCTGGCCGTCTGTGAG 735
           || | |||| || |||||| | || | ||||| |||| ||| ||| |||| || ||||||||
Db   604 GTAGACAACGGCTGGTCTGTGGAATGACATCCTCCTGCCAAGCTTCCCAAGCTTCCCACACACGGTCTCTGCGAG 663

Qy   736 TTCCCTATCTGA 747
           ||||||| ||||
Db   664 TTCCCAGCCTGA 675

RESULT 13
US-09-960-352-11785 Application US/09960352
; Sequence 11785, Patent No. US2002013719A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing

; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11785
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 50-LIB34-061-Q1-E1-B6
US-09-960-352-11785

Query Match   29.7%;   Score 222; DB 9; Length 419;
Best Local Similarity   78.3%;   Pred. No. 6e-62;
Matches 307; Conservative   0; Mismatches 75; Indels   10; Gaps   3;

Qy   1 ATGTCCCGTTCCATCACTCCCTCCTTCTCCTGAGTATGGTGGCAGCGTCTT----- 55
           |||| | |||| ||||| || | | | ||| | |||||||||||||||
Db   31 ATGTCGCTGTTTACATCACTTCCTTTTCTTCTCCTGACTGCGGTGACAGCATCTTGTGCA 90

Qy   56 -ACTCAGAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCCCAGTGATTGCCTGT 114
            |||||||||||||| |||||||| |||| | |||||||||||| ||||||||||||||||
Db   91 GACACAGAAACAGAGAACTGTGAGAACATCCGGAAGACCTGCC---CCGTGATTGCCTGT 147

Qy   115 AGCTCTCCAGGCATCAACCGCTTCCCAGGCAAGATGGGCGTGATGGCCAAGGGAGAA 174
           || |||||||||||| | | | ||||| | ||||||||| |||||| |||||||||
Db   148 GGTCCTCCGGGCATCAATGGCATCCCAGGCAAAGATGGGCGTGATGGTGCCAAGGGAGAA 207

Qy   175 AAGGGGGAACCAGGCCAAGGCTCAGAGAGGCTTACAGGGCCCCCCCTGGAAAGTTGGGGCCT 234
           ||||||||||||| ||||| || |||||| ||| ||||||||||| ||||||||||||||
Db   208 AAGGGAGAACCAGTCAAGGGCTCGCAGAGGCTCAGGGGGCCCCCCCTGGAAAGATGGGGCCT 267

Qy   235 CCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGA 294
           ||||||| ||||| || |||| || ||||||||||||| |||||| ||||| |||||||
Db   268 CAAGGAACGCCAGGGATCCCTGGGATACCAGGACCAGGACCAATAGGCCAATAGGAGGAGACCCTGGA 327

Qy   295 AAAAGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAA-GAAAAGTCTGCAAACAGA 353
           ||||||| ||| |||| || | |||||||| || |||| |||||||||| |||||||
Db   328 GAAAATATGGGTGACTATATTCGCCTGGCTACCTTAAAAAGGAGCAATTCTACAATCTGA 387

Qy   354 AATGGCACGTATCAAAAAGTGGCTGACCTTCT 385
           |||| ||| || ||||||| | |||| |||||
Db   354 AATGGCACGTATCAAAAAGTTGGCTGACCTTCT 385

Qy   388 ATTGAACCAGATCAAAAAACTGGCTAATCTTCT 419
           |||||||| |||||||||||||||||| |||||
Db   388 ATTGAACCAGATCAAAAAACTGGCTAATCTTCT 419

RESULT 14
US-10-450-472-58 Application US/10450472
; Sequence 58, Publication No. US20040132094A1
; GENERAL INFORMATION:
; APPLICANT: Borean Pharma A/S
; TITLE OF INVENTION: Combinatorial libraries of proteins having the scaffold structur
; TITLE OF INVENTION: of C-type lectin-like domains
; FILE REFERENCE: BOR00003/WO
; CURRENT APPLICATION NUMBER: US/10/450,472
; CURRENT FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8)..(400)
; OTHER INFORMATION: Rat PrMBP insert
US-10-450-472-58

Query Match   24.9%;   Score 186.2; DB 19; Length 405;
Best Local Similarity   68.5%;   Pred. No. 3.4e-50;

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Matches  257;  Conservative  0;  Mismatches  118;  Indels  0;  Gaps  0;

Qy   366 CAAAAAGTGGCTGACCTTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAA 425
             |||||| |||||| ||| |||||||| || ||||| |||||||||||||||||||||||
Db    19 CAACAAGTTGCATGCCTTCTCCATGGGTAAAAAGTCTGGGAAGAAGTTCTTTGTGACCAA 78

Qy   426 TGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGT 485
             |||||  ||| |||| |||||| |||||||||||||| |||| | | |||| |
Db    79 CCATGAAAGGATGCCCCTTTTCCAAAGTCAAGGCCCTGCTGTCCAGAGCTCCGAGGCACTGT 138

Qy   486 GGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAAGC 545
             |||||  ||  || |||||||||| ||| ||||||| ||||||| ||||||| ||||
Db   139 GGCTATCCCCAAGAATGCTGAGGAGAACAAGGCCATCCAAGAAGTGGCTAAAACCTCTGC 198

Qy   546 CTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATAG 605
             |||||||||||  ||| | ||| ||  |||  || ||||| |||| |||||| |||||
Db   199 CTTCCTAGGCATCACCGACGAGGTGACTGAAGGCCAATTCATGTGACAGGGGGGAG 258

Qy   606 ACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAAATGCTGGTTCTGATGAAGATTG 665
             |||| ||||||  ||| ||||||  || |||||| ||||| || ||||||||||||||||
Db   259 GCTCACCTACAGCAACTGGAAAAAGATGAGCCCAATGACCATGGCTCTGGGGAAGACTG 318

Qy   666 TGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCCCATCCCCATCCTGGC 725
             ||| ||||||||  ||  ||| |||| || ||||| ||||| ||
Db   319 TGTCACTATAGTAGACAACGGTCTGTGGAATGACACATCTCTGGAATCCCTGCCCAAGCTTCCACACGGC 378

Qy   726 CGTCTGTGAGTTCCC 740
             |||||||||||||||
Db   379 TGTCTGCGAGTTCCC 393


; NAME/KEY: misc_feature
; LOCATION: (425)..(425)
; OTHER INFORMATION: n is a nucleotide selected from a, g, c, or t
US-10-070-415A-45

Query Match         24.9%;  Score 186;  DB 18;  Length 1802;
Best Local Similarity  98.9%;  Pred. No. 7.8e-50;
Matches 186;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

Qy     1 ATGTCCCTGTTCCATCACTCCCTCTCCTGAGTATGGCGAGCGTCTTACTCA 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   715 ATGTCCCTGTTCCATCACTCCCTCTCCTGAGTATGGGCGAGCGTCTTACTCA 774

Qy    61 GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCCGTGCGATTGCCTGTAGCTCT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   775 GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCCGTGCGATTGCCTGTAGCTCT 834

Qy   121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGGCCACCAAGGGAGAAAAGGGG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   835 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGGCCACCAAGGNAGAAAAGGGG 894

Qy   181 GAACCAGG 188
           ||||||||
Db   895 GAACCAGG 902


Search completed: June 20, 2005, 19:30:53
Job time : 1646 secs


RESULT 15
US-10-070-415A-45
; Sequence 45, Application US/10070415A
; Publication No. US2004043379A1
; GENERAL INFORMATION:
;   APPLICANT: HASHIMOTO, Koji
;   APPLICANT: ASHIMOTO, Michie
;   APPLICANT: MISHIRO, Shunji
;   APPLICANT: OOTA, Yasuhiko
;   TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE
;   FILE REFERENCE: 220633US2SRDPCT
;   CURRENT APPLICATION NUMBER: US/10/070,415A
;   CURRENT FILING DATE: 2003-07-23
;   PRIOR APPLICATION NUMBER: PCT/JP02/02030
;   PRIOR FILING DATE: 2002-03-05
;   PRIOR APPLICATION NUMBER: JP 2001-090053
;   PRIOR FILING DATE: 2001-03-27
;   PRIOR APPLICATION NUMBER: JP 2001-284112
;   PRIOR FILING DATE: 2001-09-18
;   NUMBER OF SEQ ID NOS: 72
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1802
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (96)..(96)
;   OTHER INFORMATION: n is a nucleotide selected from a, g, c, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (649)..(649)
;   OTHER INFORMATION: n is a nucleotide selected from a, g, c, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (868)..(868)
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;   NAME/KEY: misc_feature
;   LOCATION: (884)..(884)
;   OTHER INFORMATION: n is a nucleotide selected from a, g, c, or t
;   FEATURE:
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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      June 20, 2005, 03:04:56 ; Search time 3223 Seconds
                                       (without alignments)
                                       8822.218 Million cell updates/sec

Title:       US-10-054-536-2
Perfect score: 747
Sequence:    1 atgtccctgttccatcact........tctgtggagtccctattctga 747

Scoring table: IDENTITY_NUC
             Gapop 10.0 , Gapext 1.0

Searched:    34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:    68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
             1: gb_est1:*
             2: gb_est2:*
             3: gb_htc:*
             4: gb_est3:*
             5: gb_est4:*
             6: gb_est5:*
             7: gb_est6:*
             8: gb_gss1:*
             9: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	678	90.8	747	9	AY413286	AY413286 Homo sapi
2	671.6	89.9	747	9	AY413287	AY413287 Pan trogl
3	668.6	89.5	1000	7	CO579105	CO579105 ILLUMIGEN
4	644.6	86.3	968	7	CO579085	CO579085 ILLUMIGEN
5	394.4	52.8	807	7	CO738739	CO738739 SILE04c21
6	352.2	47.1	735	9	AY413288	AY413288 Mus muscu
7	338.6	45.3	977	1	CO583176	CO583176 ILLUMIGEN
8	335	44.8	828	2	BF537636	BF537636 602054416
c 9	324.8	43.5	722	7	CK778513	CK778513 965675 MA
10	303	40.6	367	1	AV660023	AV660023
11	302.2	40.5	657	1	AI255533	AI255533 ui55f12.y
12	301.4	40.3	1162	3	AY325174	AY325174 Rattus no
13	301.4	40.3	1162	3	AY325178	AY325178 Rattus no
c 14	292.4	39.1	869	1	AI195233	AI195233 ui62c03.x
15	291	39.0	367	1	AV660367	AV660367 AV660367
c 16	290.4	38.9	789	1	AI174038	AI174038 ud67a02.x
17	286	38.3	1565	3	AK034788	AK034788 Mus muscu
18	283.6	38.0	772	7	CO812153	CO812153 AGENCOURT
19	276	36.9	896	5	CO809875	CO809875 AGENCOURT
20	268.4	35.9	557	2	BE682267	BE682267 180230 MA
21	268	35.9	788	4	BI147944	BI147944 602912658
c 22	267.6	35.8	784	1	AI173576	AI173576 ud68d03.x
c 23	258.4	34.6	777	1	AI194713	AI194713 ui55f12.x
c 24	257	34.4	956	6	CA479090	CA479090 AGENCOURT

25	256.6	34.4	664	1	AI876217	AI876217 uj59d03.y
26	256	34.3	592	1	AI786738	AI786738 uj56d08.x
c 27	255.6	34.2	832	6	CB948709	CB948709 AGENCOURT
28	250.2	33.5	957	6	CA478654	CA478654 AGENCOURT
29	248.2	33.3	627	7	CF179019	CF179019 813103 MA
30	246.2	33.0	738	7	BI144334	BI144334 602308384
31	245.8	32.9	540	5	BX526094	BX526094
32	243.4	32.6	753	4	BI145807	BI145807 602909275
33	242.6	32.5	799	1	AI097858	AI097858 ue40g03.y
34	242.2	32.4	653	7	CO675645	CO675645 DG42-172i
c 35	242	32.4	566	7	CO775884	CO775884 ILLUMIGEN
36	240.4	32.2	949	6	CA479163	CA479163 AGENCOURT
c 37	239.8	32.1	677	1	AI118440	AI118440 ue40g03.x
38	239.4	32.0	476	2	BF652528	BF652528 276116 MA
39	239	32.0	653	6	CB419261	CB419261 592111 MA
c 40	236.4	31.6	605	7	CO676106	CO676106 DG42-184f
41	236.4	31.6	758	1	AV649316	AV649316
c 42	235.8	31.6	619	7	CO674631	CO674631 DG42-144g
43	234.8	31.4	393	1	AV649531	AV649531 AV649531
c 44	234	31.3	611	7	CO674696	CO674696 DG42-146b
45	231.6	31.0	760	6	CB947613	CB947613 AGENCOURT

ALIGNMENTS

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RESULT 1
AY413286
AY413286
LOCUS       AY413286          747 bp    DNA    linear    GSS 17-DEC-2003
DEFINITION  Homo sapiens MBL2 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY413286
VERSION     AY413286.1  GI:39769248
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE       Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL     Science 302 (5652), 1960-1963 (2003)
PUBMED      14671302
REFERENCE   2  (bases 1 to 747)
AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE       Direct Submission
JOURNAL     Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES            Location/Qualifiers
     source         1..747
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
     gene           <1..>747
                    /gene="MBL2"
                    /locus_tag="HCM4840"
ORIGIN

Query Match             90.8%;  Score 678;  DB 9;  Length 747;
Best Local Similarity   90.8%;  Pred. No. 1.4e-182;
Matches  678;  Conservative  0;  Mismatches  69;  Indels  0;  Gaps  0;

Qy         1 ATGTCCCTGTTCCATCACTCCCTCCCTTCCTTCCTCGTGAGTATGGTGGCAGCCGTCTTACTCA 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
     Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
     Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
     Adams,M.D. and Cargill,M.

TITLE   Direct Submission

JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
     Rockville, MD 20850, USA

COMMENT   This sequence was made by sequencing genomic exons and ordering
     them based on alignment.

FEATURES   Location/Qualifiers

     source   1..747
                  /organism="Pan troglodytes"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:9598"

     gene   <1..>747
                  /gene="MBL2"
                  /locus_tag="HCM4840"

ORIGIN

Query Match   89.9%;   Score 671.6;   DB 9;   Length 747;
Best Local Similarity   90.2%;   Pred. No. 9.6e-181;
Matches 674;   Conservative   0;   Mismatches 73;   Indels   0;   Gaps   0;

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Qy    1 ATGTCCCGTTCCATCACTCCCTTCCTTCCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGTCCCGTTCCATCACTCCCTTCCTTCCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60

Qy   61 GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCCAGTGATTGCCTGTAGCTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GAAACTGTGACCTGTGAGGATGCCCAAAGACCTGCCCTGCCAGTGATTGCCTGTAGCTCT 120

Qy  121 CCAGGCATCAACGCTTCCCAGGCAAAGATGGGCGTGATGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CCAGGCATCAACGCTTCCCAGGCAAAGATGGGCGTGATGGCGTGATGGCACCAAGGGAGAAAAGGGG 180

Qy  181 GAACCAGGCCAAGGGCTTACAGGGCCTCCAGGA 240
          |||||||||||||||||||||||||||||||||
Db  181 GAACCAGGCCAAGGGCTTACAGGGCCTCCAGGA 240

Qy  241 AATCCAGGGCCTTCTGGGTCACCAGGACCCAAAAGGGCCAAAAGAGGAGACCCTGGAAAAGT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AATCCAGGGCCTTCTGGGTCACCAGGACCCAAAAGGGCCAAAAGAGGAGACCCTGGAAAAGT 300

Qy  301 CCGGATGGTGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAGAATGGCA 360
          |||||
Db  301 CCGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 360

Qy  361 CGTATCAAAAAGTGGCTGACCTTCTCTCGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
          |||||||
Db  361 NNNNNNNNNNNNNGGCTGACCTTCTCTCGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420

Qy  421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTGTGTCAAGTTCAAGTTCAAGGCC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTGTGTCAAGTTCAAGTTCAAGGCC 480

Qy  481 TCTGTGGCCACCCCAGGAAATGCTGCAGAATGCTGCAGAATCTCATCAAGGAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TCTGTGGCCACCCCAGGAAATGCTGCAGAATGCTGCAGAATCTCATCAAGGAG 540

Qy  541 GAAGCCTTCCTGGCATCATCACTGATGAGAGAACAGAGAGGGCAGTTTCGTGGATCTGACAGGA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 GAAGCCTTCCTGGCATCATCACTGATGAGAGAACAGAGAGGGCAGTTTCGTGGATCTGACAGGA 600

Qy  601 AATAGACTGACCTACACAAACTGAACCGAGGTGAACCCAACAATGCTGGTTCTGATGAA 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 AATAGACTGACCTACACAAACTGAACCGAGGTGAACCCAACAATGCTGGTTCTGATGAA 660

Qy  661 GATTGTGTATTGCTACTGAAAAAATGGCCAGTGAATGACGTCCCCTGCTCCACCTCCCAT 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 GATTGTGTATTGCTACTGAAAAAATGGCCAGTGAATGACGTCCCCTGCTCCACCTCCCAT 720

Qy  721 CTGGCCCGTCGTGTGAGTTCCCTATCTGA 747
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RESULT 2

AY413287

LOCUS   AY413287   747 bp   DNA   linear   GSS 17-DEC-2003

DEFINITION   Pan troglodytes MBL2 gene, VIRTUAL TRANSCRIPT, partial sequence,
     genomic survey sequence.

ACCESSION   AY413287

VERSION   AY413287.1   GI:39769249

KEYWORDS   GSS.

SOURCE   Pan troglodytes (chimpanzee)

ORGANISM   Pan troglodytes
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE   1 (bases 1 to 747)

AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
     Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
     Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
     Adams,M.D. and Cargill,M.

TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
     gene trios

JOURNAL   Science 302 (5652), 1960-1963 (2003)

PUBMED   14671302

REFERENCE   2 (bases 1 to 747)

RESULT 3

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Db  721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
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LOCUS   CO579105   1000 bp   mRNA   linear   EST 20-JUL-2004
DEFINITION ILLUMIGEN MCQ_50626 Katze_MNLV Macaca nemestrina cDNA clone
            IBIUW:18533 5' similar to Bases 76 to 977 highly similar to human
            MBL2 (Hs.2314), mRNA sequence.
ACCESSION   CO579105
VERSION   CO579105.1 GI:50409981
KEYWORDS   EST.
SOURCE   Macaca nemestrina (pig-tailed macaque)
  ORGANISM Macaca nemestrina
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1 (bases 1 to 1000)
  AUTHORS   Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
  TITLE   Large-scale Rhesus Macaque cDNA Sequencing
  JOURNAL   Unpublished (2003)
COMMENT   Contact: C. Magness
            Illumigen Biosciences Inc.
            2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
            Tel: 2063780400
            Fax: 2063780408
            Email: cmagness@illumigen.com
            Sequenced on 2004.07.16. 690 Q20 bases. Library Preparation: Prof.
            Michael Katze Lab at University of Washington DNA Sequencing:
            Illumigen Biosciences Inc. For further information, see
            http://www.macaque.org
            PCR Primers
            FORWARD: CCCTCACTAAAGGGAACAAAA
            BACKWARD: CACTATAGGGCGAATTGGGTA
            Insert Length: 1000 Std Error: 0.00
            Plate: CL000535 row: B column: 08
            Seq primer: CCCTCACTAAAGGGAACAAAA
            POLYA=Yes.
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                     /mol_type="mRNA"
                     /strain="Indian"
                     /db_xref="taxon:9545"
                     /clone="IBIUW:18533"
                     /sex="male"
                     /lab_host="Electromax DH10B"
                     /clone_lib="Katze_MNLV"
                     /note="Organ: liver; Vector: pDONR 222; Site_1: BsrG I;
                     Site_2: BsrG I; Created from CloneMiner cDNA_Library
                     Construction kit (catalog #18849-029)"
ORIGIN

Query Match   89.5%; Score 668.6; DB 7; Length 1000;
Best Local Similarity 93.4%; Pred. No. 7.6e-180;
Matches 698; Conservative   0; Mismatches   49; Indels   0; Gaps   0;

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Qy    1 ATGTCCCTGTTCCATCACTCCCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA  60
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Qy   61 GAAACTGTGACCTGTGAGGATGCCAAAAGACCTGCCCTGCCAGTGATTGCCTGTAGTCT 120
        ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  147 GAAACTGTGACCTGTGAGGATTCCCAAAAGATTCTGCCCTGCCGTGTGATTGCCTGTAACTCC 206

Qy  121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCCACCAAGGGAGAAAGGGG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  207 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCCACCAAGGGAGAAAAGGGG 266

Qy  181 GAACCAGGCCAAGGGCTTACAGGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  267 GAACCAGGCCAAGGGCTTCAGAGGGTTTACAGGGCCCTCCTGGAAAGTTGGGGCCTCCAGGA 326
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LOCUS   CO738739   807 bp   mRNA   linear   EST 29-JUL-2004
DEFINITION   SlLR04c21f10f1 squirrel embryo library 1 Spermophilus lateralis
             cDNA clone 21f10 5', mRNA sequence.
ACCESSION   CO738739
VERSION   CO738739.1 GI:50826009
KEYWORDS   EST.
SOURCE   Spermophilus lateralis (golden-mantled ground squirrel)
ORGANISM   Spermophilus lateralis
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
             Spermophilus.
REFERENCE   1 (bases 1 to 807)
AUTHORS   Williams,D.R., Gracey,A.Y., Martin,S.L., Hughes,M.A., Li,W.,
             Rogers,J. and Cossins,A.R.
TITLE   Microarray analysis of transcriptional changes during hibernation
             in the golden mantled ground squirrel, Spermophilus lateralis
JOURNAL   Unpublished (2004)
COMMENT   Contact: Andrew R. Cossins
             Laboratory for Environmental Gene Regulation
             University of Liverpool
             School of Biological Sciences, The Biosciences Building, Crown
             Street, Liverpool, United Kingdom, L69 72B
             Tel: +44(0)151-795-4510
             Fax: +44(0)151-795-4431
             Email: cossins@liv.ac.uk
             Vector has been trimmed from this EST.
             Plate: 21 row: f column: 10
             Seq primer: pflc T7 (5'-AATACGACTCACTATAGGG-3')
             High quality sequence stop: 807.
FEATURES   Location/Qualifiers
     source   1..807
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                     /db_xref="taxon:76772"
                     /clone="21f10"
                     /sex="male and female"
                     /tissue_type="embryo"
                     /dev_stage="embryonic"
                     /lab_host="E.coli Electromax DH10B"
                     /clone_lib="squirrel embryo library 1"
                     /note="Vector: pflc; Site 1: SalI GTCGAG; Site 2: BamHI
                     GGATCC; Normalized and subtracted cDNA library prepared
                     from embryos"
ORIGIN

Query Match   52.8%; Score 394.4; DB 7; Length 807;
Best Local Similarity   73.5%; Pred. No. 2.3e-101;
Matches 548; Conservative   0; Mismatches 186; Indels 12; Gaps 3;

Qy   1 ATGTCCCTGTTTCCATCACTCCCTCCCTTCTCCTGAGTATGGTGCAGCGTCTTACTCA 60
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Db   64 ATGTCCCTGTTTCCATTACTCCCTGTCTTTTCCTGAGTGTGGTGGTGGACAGTCGC---CTCA 120

Qy   61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCCAGTGATTGCCTGTAGCTCT 120
          ||||||||||||||||||||||||||||||||||||||||||||| ||||---|||||||||
Db   121 GAAACAAAAACATGTGAGGATGCCCAGAAGACCTGCTCT---GTGATTACCTGTGGGATC 177

Qy   121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
          |||||||||||||||||||||||||| |||| ||||||||||||||||||||||||||||||
Db   178 CCTGTCACCAACGGACTCCAGGCAGAGATGGGCGAGATGGACTCAAGGAGAAAAGGGA 237

Qy   181 GAACCAGGCCAAGGGCTTCAGGAGCTTACAGGGCCCCCCTGGAAAAGT 240
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   238 GAGCCAGGGCCTCAGGGGCTCAGAGGTTGCAGGGCCCTCCAGGGAAACTCGGGGCCTCCAGGA 297

Qy   241 AATCCAGGGCCTTGAGGATGCCAAAAGAGAAATGGCA 300
          ||||||||||||||||||||| ||||||||||||||||
Db   298 AATCCAGGGCCTTGGTGGGCTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGAAAAAGT 357

Qy   301 CCGGATGTGATAGTAGCCTGGCTAACCTGGCTAACTGACTTAGAGAGAGATAAGGAACCTGAAATCAGAA 417
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Db   358 TCGGCTGCTGAGACTAAACTGGCTAACTGGCTAACTTAGAGAGAGATAAGGAACCTGAAATCAGAA 417

RESULT 5
CO738739

Tue Jun 21 12:43:45 2005

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                     /sex="male"
                     /lab_host="Electromax DH10B"
                     /clone_lib="Katze MNLV"
                     /note="Organ: liver; Vector: pDONR 222; Site 1: BsrG I;
                     Site 2: BsrG I; Created from CloneMiner cDNA Library
                     Construction kit (catalog #18249-029)"
ORIGIN

Query Match   86.3%; Score 644.6; DB 7; Length 968;
Best Local Similarity   93.2%; Pred. No. 5.6e-173;
Matches 696; Conservative   0; Mismatches 49; Indels 2; Gaps 2;

Qy   1 ATGTCCCTGTTTCCATCACTCCCCTCCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
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Db   94 ATGTCCCTGTTTCCATCACTCACTCCTCCCTTCTCCTGAGTGTGGTGGTGGCAACATCTTACTCA 153

Qy   61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCCAGTGATTGCCTGTAGCTCT 120
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Db   154 GAAACTGTGACCTGTGAGGATTCCCAAAAGATCTGCCCTGCGGTGATTGCCTGTAACTCC 213

Qy   121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
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Db   214 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCGTGATGGCGTGCCACCAAGGGAGAAAAGGGG 273

Qy   181 GAACCAGGCCAAGGGCTTCAGGAGCTTACAGGGCCCCCCTGGAAAAGT 240
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Db   334 AATCCAGGGTCTTCTCGGGTCACCAGGACCAAAAGGGCCAAAAGGGAGAGAGT 393

Qy   301 CCGGATGTGATAGTAGCCTGCTGCCTCAGAAAGAAAAAGCTCTGCAAACAGAAATGGCA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   394 CCAGATTGTGAGAGTAGCCCTGCGTGCCTCAGAAAGAAAAAGCTCTGCAAACAGAAATGGCT 453

Qy   361 CGTATCAAAAAGTGGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   454 CGTATCAAAAAGTGGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 513

Qy   421 ACCAATGTGAAATAATAATGACCTTTGAAAAAGTGAAGGCTTGTGTGTCAGGTCAGGCC 480
          ||||||||||||||||||||||||| ||| |||||||||||||||||||||| |||||||
Db   514 ACTAATGTGAAATGATGATGACCTTTGACAAAGTGAAGGCCCGTGTGTCCGAGTTCAGGCC 573

Qy   481 TCTGTGGCCACCCCCAGGAAATGCTGCAGGAATGCTGCAGAGGAATGCTGAGAGAATGTGA 540
          |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   574 TCTGTGGCCACCCCCAGGAAATGCTGCAGGAATGCTGCAGAGGAATGTGAGAGAATGTGA 633

Qy   541 GAAGCCTTCCTGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTTGGATCTGACAGGA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   634 GAAGCCTTCCTGGCATCACTGATGAGAAGACAGAAGGGGAGTTTGTAGATCTGACAGGA 693

Qy   601 AATAGACTGACCTACACAAACTGGAACCAGCAGGGTGAACCCAACAAGTCTGGTTCTGATGAA 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   694 AATAAACTGACCTACACAAACTGGAACCAGCAGGGTGAGCCC-ACAAGTCTGGTTCTAATGAG 752

Qy   661 GATTTGTGTATTGCTACTGAAAAATGGCCAGTGAATGACGTCTCCCCTGCTCACCTCCCAT 720
          |||||||||||||||| ||||||||||||||||||||| |||||||||||||||||||||||
Db   753 AACTGTGTATTGTTACTG-AAAATGGCAAGTGAATGACATCCCCTGCTCCTCCCTTCCCAT 811

Qy   721 CTGGCCGTCGTGTGAGTTCCCTATCTGA 747
          ||||||| |||||||||||||||||||||
Db   812 CTGGCCCCTCGCGGATTTCCCTATCTGA 838

```
Qy    355 ATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGCAAACAAGTTGGAACAAGTTC 414
          ||| ||| |||||||||||||||||||||||||||||| |||| ||||||||||||||
Db    418 TTGGACCGCATTAAAAAGTTGCAAGCCTTCTCTTGGCAAAAAGTCTGGAAAGAAGTTC 477

Qy    415 TTCCTGACCAATGGTGAAATAATGACCTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTC 474
          |||||||||||||||||||| ||| ||||||||| ||| ||||||||||||||||
Db    478 TACGTGACCAATGGTGAAAATATGCCTTTTCCAAAGCGAAGGCTTGGTGTGCACAGAGCTC 537

Qy    475 CAGGCCTCTGTGGCCACCCCCCAGGAATGCTGCAGAGAATGCCATTCAGAATCTCATC 534
          |||| |||||||||||||| ||||||||| ||| ||||| ||| ||||||||||
Db    538 CAGGCCACTGTGCTGCCCCCAAGAATGTCTGAGGAGACAACGAACATCCAACAGGTGGCC 597

Qy    535 AAGGAGGAAGCCTTCCTGGGCATCACTGATGATGAGAAGAGACAGAGTTGTGGATCTG 594
          | ||| |||||| |||||| ||| |||||| |||||||||||||||||||
Db    598 AGAGACAAATGTCTTCCTGGGTATCACAGATGAGGAGGTTACAGAAGGCCAGTTTATGTATGTG 657

Qy    595 ACAGGAAATAGACTGACCTACACAAACTGGACGAGGTGACCCACAAATGCTGGTTCT 654
          |||||||| ||| |||||||| || |||||||||||| ||||| ||| ||||||||
Db    658 ACAGGAGGAGCCTAACCTACACAGACCTGGAGGGCGAATGAGCCTAATAACCATGGCTCA 717

Qy    655 GATGAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACC 714
          || ||| ||||| |||||| |||| |||||||| ||| ||||| ||||||||||||
Db    718 GGGGAGGACTGTGTGATTCTCTTGAAGGATGACTCTCGGAATGATGTTTCCTGCTCGTCC 777

Qy    715 TCCCATCTGGCCGTCTGTGAGTTCCC 740
          ||| ||| |||||||||||||||||
Db    778 TCCTTCCCTGGTGTCTGTGAGTTCCC 803
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Qy     26 TCCTTCCTGAGTATGTGGCAGCGTCTTACTTGTGACCTGTGAGGATGCCC 85
          ||||||||| |||||||||||||||| |||||||||||||||| ||||||
Db     20 TCCTTCTGCTGTGTGTGTGTGCACAGTGGTTATGCAGAGACCTTAACC---GAAGGTGTTC 76

Qy     86 AAAAGACCTGCCCTGCCAGTGATTGCCTGTAGCTTCCAGGCATCAACGGCTTCCCAGGCA 145
          |||| |||||| |||||||  |||||||| ||| ||| ||||||||||||||||||||||
Db     77 AAAATTCCTGCCCT---GTGGTTACCTGCCAGTTCCCAGGCCTTCCAGCCTGAATGCATCCCCAGCA 133

Qy    146 AAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGGAACCAGCCAAGGGCTCAGAGGCT 205
          |||||||| |||||||| ||||||||||||| |||||||||||||||||||||||||
Db    134 AAGATGGACGTGACGGCGTGCCAAGGAGAGAAAAGGGAGAACCAGGTCAAGGGCTCAGAGGCT 193

Qy    206 TACAGGGCCCCCCTGGAAAGTTGGGCGGCCTTCCAGGAAATCCTGGGCTTCGGGTCACCAG 265
          ||||||  ||||||||||||||  ||| |||||||||||||  |||||||||||||||
Db    194 TGCAAGGCCCTCCTGGAAAAGTAGGACCTTCAGGAGACCCCCAGGGAATCCGGGTTAAAAG 253

Qy    266 GACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGTCCGGATGGTGATAGTAGCCTGGCTG 325
          |||| |||| | |||| |||||||| ||||||||  ||||  || |||||||||||||||
Db    254 GAGCAGTGGGACCGGTCCGAAAGGACCAGCCGTGGGACGACAGAGCAGNNNNNNNNNNNNN 313

Qy    326 CCTCAGAAAGAAAAAGCTTCGCAAACAGAAATGGCACGTATCAAAAAGTGGCTGACCTTCT 385
          |||||||||||||||  ||||||||||||||||||||||||||||||
Db    314 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGGTGCTCTTCT 373

Qy    386 CTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAATGGTGAAATAATGACCTTTG 445
          ||||| ||||| |||||||  ||||||||| |||| ||| ||||| |||| ||||||||
Db    374 CTCTGAGTGAAAAAGTTGGAAAGAAGAAGTATTTTGTGAGCAGTGTTAAAAAGATGAGCGCTTG 433

Qy    446 AAAAAGTGAAGGCCTTGTGTGTCAAGTTCAGGCCTCTGTGGCCACCCCCAGGAATGCTG 505
          ||| |||||||| ||||||||||||||||||||| ||||||||||||||||||
Db    434 ACAGAGTGAAGGCCCTGTGTCCTGCCAGGCTCTGTGGGCCACTCCCAGGAATGCTG 493

Qy    506 CAGAGAATGAGAGCCATTCAGAATCTCATCAAGGAGGAGGAGCCTTCCTGGGCATCACTGATG 565
          |||||||||| ||||| |||||||||||||| |||||||||||||||||||| |||||||||||
Db    494 AGGAAAACTCGGCATCCAGAAAGTGGCCAAAGATATTGCCTATTGGGCATCACAGATG 553

Qy    566 AGAAGACAGAAGGGCAGTTTGGATCGAGAAGAAATAGACTGACCTACACAAACTGA 625
          ||| |||||  ||||||||| |||| |||| ||||||||||||| ||| ||||||
Db    554 TGAGGGTTGAAGGCAGTTTTGAGGATCTGACAGGAGGAAACAGAGTGCGGTATACTAATTGGA 613

Qy    626 ACGAGGTGAACCCAACAAATGCTGGTTCTGATGAAGATTGTGTATTGCTACTGAAAAATG 685
          ||||||||||||||||||||||||||  |||| ||  ||||| |||| ||||||||||||
Db    614 ATGATGGGGAGCCCAACACGGGGGGATGGGGGAAGACTGTGTGGTGATCTTGGGAAATG 673

Qy    686 GCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTGGCCGTCTGTGAGTTCCCTATCT 745
          ||| |||||| ||||||||| |||  ||||| ||| |||||||||||||||||||||
Db    674 GCAAGTGAACGATGTCCCCTGCTCTCTGACTCTTTTTTGGCAATCTGTGAATTCTCTGACT 733

Qy    746 GA 747
          ||
Db    734 GA 735
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RESULT 7
CO583176

LOCUS   CO583176   977 bp   mRNA   linear   EST 20-JUL-2004
DEFINITION   ILLUMIGEN MCQ_44503 Katze_MMLV Macaca mulatta cDNA clone
             IBIUW:18650 5' similar to Bases 266 to 879 highly similar to human
             Unigene Hs.102310, mRNA sequence.
ACCESSION   CO583176
VERSION   CO583176.1   GI:50415779
KEYWORDS   EST.
SOURCE   Macaca mulatta (rhesus monkey)
ORGANISM   Macaca mulatta
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
             Cercopithecinae; Macaca.
REFERENCE   1 (bases 1 to 977)
AUTHORS   Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
TITLE   Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL   Unpublished (2003)
COMMENT   Contact: C. Magness

RESULT 6
AY413288

LOCUS   AY413288   735 bp   DNA   linear   GSS 17-DEC-2003
DEFINITION   Mus musculus MBL2 gene, VIRTUAL TRANSCRIPT, partial sequence,
             genomic survey sequence.
ACCESSION   AY413288
VERSION   AY413288.1   GI:39769250
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 735)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
             gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE   2 (bases 1 to 735)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
TITLE   Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
             Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
             them based on alignment.
FEATURES   Location/Qualifiers
     source   1..735
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene   <1..>735
                     /gene="MBL2"
                     /locus_tag="HCM4840"
ORIGIN

Query Match   47.1%;   Score 352.2;   DB 9;   Length 735;
Best Local Similarity 66.3%;   Pred. No. 2.7e-89;
Matches 479;   Conservative 0;   Mismatches 237;   Indels 6;   Gaps 2;

```
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.06.17. 631 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org
PCR Primers
FORWARD: CCCTCACTAAAGGGAACAAAA
BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 977  Std Error: 0.00
Plate: CL000398 row: C column: 06
Seq primer: CCCTCACTAAAGGGAACAAAA
POLYA=No.

FEATURES       Location/Qualifiers
     source    1..977
               /organism="Macaca mulatta"
               /mol_type="mRNA"
               /strain="Indian"
               /db_xref="taxon:9544"
               /clone="IBIUW:18690"
               /sex="female"
               /dev_stage="adult"
               /lab_host="Electromax DH10B"
               /clone_lib="Katze MMLV"
               /note="Organ: liver; Vector: pDONR 222; Site_1: BsrG I;
               Site_2: BsrG I; Created from CloneMiner cDNA Library
               Construction kit (catalog #18249-029)"

ORIGIN

Query Match     45.3%;  Score 338.6;  DB 7;  Length 977;
Best Local Similarity  72.5%;  Pred. No. 2.3e-85;
Matches  469;  Conservative  0;  Mismatches  169;  Indels  9;  Gaps  2;

Qy    1 ATGTCCCTGTTTCCATCACTCCCTTCCTTCCTCCTGAGTATGGTGCAGCGTCTTACTCA 60
          ||||||||||||| |||||||| || ||| ||||||  |||| | ||||||  ||
Db   85 ATGTTCCTGTTTTCCGTCATTCCGTCCTTCCTCGTGTGTCTGTGGTGACAGCTTCCTGCTCC 144

Qy   61 GAAACTGTGACCTGTGAGGATGCCAAAAGACCTGCCCTGCCAGTGATTGCTGTAGCTCT 120
          |||||  ||||||||||||||||||||||||
Db  145 GAAACAAAAGCCTGGACGATGCCCAGAAGACCTGCTCT---GTGATTACCTGTGCATC 201

Qy  121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCGACCAGAGGAGAAAAGGGG 180
Db  202 CCCGTCACCAATGGCACCCCAGGCAGAGATGGGCGAGATGGCGAGATGGACCCAAGGGGAAAAGGGA 261

Qy  181 GAACCAGCCAGGGGCTCGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
Db  262 GAGCCCAGTGCAAGGGCCTCAGAGGTTGCAGGGGTCGCAGGAGTCGGGGCCCCCAGGA 321

Qy  241 AATCCAGGGGCCTTCGGGTCACCAGGACCAAAAGGGCAAAAGGAGACCCTGGAAAAAGT 300
Db  322 AACACAGGGGCGTTCTGGAATTCCAGGACCAAGGGACCAAGGAGAGATCATGGGACAAT 381

Qy  301 CCCGGATGGTGATAGTAGCTGTCGGCTGCCTCAGAAGAAAGCT------CTGCAAAACAGAA 354
Db  382 TCAGTTGCTGAGGCTAAGCTGCCCAACTTAGAGACAGCCTACAGAGACAAGTTC 441

Qy  355 ATGGCACGTATCAAAAAGTGGCTGACCTTCTTCTCTGGGCAAACAAGTTGGGAACAAGTTC 414
Db  442 CTGGACCCACATGGAGGACAGTGCAAGCGTGAAATGTCTGGGAAGAGAAGTC 501

Qy  415 TTCCTGACCAATGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTC 474
Db  502 TTCTGGACCAAGCGTGAGCGGATGCCTTTTCTCCGAAGTGAAGGCTCTGTTGCTGTGGGCTC 561

Qy  475 CAGGCCTTCTGTGGCCACCCCCAGGAATGCTGCAGGAATGACGAGCCATTCAGAATCTCATC 534
Db  562 CAGGCCACGTGGCTGCTGCCCCAAGGAATGCCCCAAGGAGAATAAGCCCATCCAGGATGTGGCC 621

Qy  535 AAGGAGGAAGCCTTCCTGGGCATCTGATGAGGAAGACAGAAGACAGCAGGGGCAGTTTGTGGATCTG 594
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Db  622 AAAGACACTGCCTTCCTGGGCATCACAGATGAGGAGGCACCGAGGCACCGAGGGTGAACCCAA 681
Qy  595 ACAGGAAATAGACTGACCTACACAACAACTGGAACTGGAACGAGGGTGAACCCAA 641
Db  682 ACGGGCGGAAGGCTGACCTACAGCAACTGGAAAAAGGATGAACCAAA 728

RESULT 8
BF537636
LOCUS       BF537636               828 bp    mRNA    linear   EST 11-DEC-2000
DEFINITION  602054516F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4193883 5',
            mRNA sequence.
ACCESSION   BF537636
VERSION     BF537636.1  GI:11625004
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 828)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey B. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9526 row: o  column: 04
            High quality sequence stop: 757.

FEATURES             Location/Qualifiers
     source          1..828
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4193883"
                     /clone_lib="NCI_CGAP_SG2"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
                     NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo
                     dT. Average insert size 1.3 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match     44.8%;  Score 335;  DB 2;  Length 828;
Best Local Similarity  71.5%;  Pred. No. 2.3e-84;
Matches  511;  Conservative  0;  Mismatches  195;  Indels  9;  Gaps  5;

Qy   34 CTGAGTATGGTGGCAGCGTCTTACTCAGAAACTGTGACCTGTGAGGATGCCAAAAGACC 93
Db    3 CTGTGTGTGGTGACAGTGGTTTATGCAGAGACCTTAACC---GAAGGTGTTCAAAATTCC 59

Qy   94 TGCCCTGCCAGTGATTGCTGTAGCTCTCCAGGCATCAACAGCGGTTCCCAGGCAAAGATGGG 153
Db   60 TGCCCT---GTGGTTACCTGCAGTTCTCCAGGCCTCAGAGGCTTCCCAGGCAAAGATGGA 116

Qy  154 CGTGATGGCGACCAGAGGAGAAAAGGGGGAACCAGCCAGGGGCTCAGAGGCTTACAGGGC 213
Db  117 CGTGACGGTGCCAAGGAGAAGGGAGAACCAAGGTCAAGGGCTCAGAGGCTTCAGAGGC 176

Qy  214 CCCCCTGGAAAGTTGGGGCCTCCAGGAAATCCAGGGGCCTTCGGGTGGAGGATGCCAAAAGACC 273
Db  177 CCTCCTGGAAAAGTAGGACCTACAGAGACCCCAGGGAATCCCGGGGTTAAAAGGAGCAGTG 236

Qy  274 GGCCAAAAGGAGACCCTGGAAAAAGTCCGGAAAAAGTCCGGATGGTGGCC 333
Db  237 GGACCGAGGAAGGAGACCGTGGGAACAGAGCAGAGATTGATTGATTCAGAA 296
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ORIGIN

Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."

```
Query Match          43.5%;   Score 324.8;  DB 7;   Length 722;
Best Local Similarity 70.5%;   Pred. No. 1.9e-81;
Matches 450;  Conservative   0;  Mismatches 182;  Indels   6;  Gaps   1;

Qy  116 GCTCTCCAGGCATCAACGGCTTCCCAGGCAAGATGGGCGTGATGGACCAAGGGAGAAA 175
            ||||||||||   || |||  |||||||| ||||||  || |||||||||||||||
Db  721 GCATCCCGTCACCAATGGCACCCCAGGCAGAGATGGGCGAGATGGGACCCAAGGGGGAAA 662

Qy  176 AGGGGGAACCAGGCCAAGGGCTCAGAGGGCTTACAGCGGGCCCCCTGGAAGTTGGGGCCTC 235
            ||||||||||| || ||| || |||||||||||| ||| ||||| || || ||||| |
Db  661 AGGGGAGAGCCCAGTCAGCAAGGGCCTCAGGGCCTCTTAGGAGGTTTGCAGGGGCCGGGGCCCC 602

Qy  236 CAGGAAATCCAGGGCGTTCTGGGTCACCAGGACCAAAAGGGCCAAAAAGGAGACCCTGAA 295
            ||||||| ||||| |||||||| ||| |||| |||||||| |||||||||||||||
Db  601 CAGGAAACACAGGGGCTCCTGGAATTCCAGGACCAAGGGGACCAAGGGGACAAAAGGAGATCATGGGG 542

Qy  296 AAAGTCCGATGTGATAGTAGCCTGGCCTCAGAGAAG------AAAAGTCTGCAAA 349
            ||| |||  ||| |  ||||| |||||||||| ||     ||||| || |||
Db  541 ACAATTCAGTTGCTGAGGCTAAGCTGGCCAACTTAGAGAGACAGTCTTAGAGAGATCATGGGG 482

Qy  350 CAGAAATGCACGTATCAAAAAGTGGCTGACCTTCTCTCGGCCAAACAAGTTGGGACA 409
            ||||||| ||||||||||||||||||| ||| || ||| ||||| |||||||||||
Db  481 CAGAACTGGACCACACATGAAGAGCTGCGAAGCCTTCTCTTCCTCTTGGGGAAAATGTCTGGGAGA 422

Qy  410 AGTTCTTCTGACCAATGTGAAATAATGACCTTTGAAAAAGTGAAGGGCCTTGTGTGTCA 469
            |||||||| |||| ||| ||||||||  ||  ||||| ||||| |||  |||| ||
Db  421 AGCTCTTCGTGACCAACGGTGCCACCCCAGGAATGCTGCAGAGATGGAGCCATTCAGAATC 362

Qy  470 AGTTCCAGGCCTTCTGTGTGCCACCCCCAGGAATGCTGCAGAGATGCTGCAGGAGATGGAGCCATTCAGAATC 529
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GGCTCCAGGCCACGGTGCGTGCCGCCCCCAGGAATGCCGAGGAGAATAAGGCCATCCAGGATG 302

Qy  530 TCATCAGGAGGAAGCCTTCCTGGGCATCACTGATGATGAAGAACAGAGAGGGCAGTTTGTGG 589
            |||  |||||| || |||| |||||| | |||| ||||| ||  ||||||||||||| ||
Db  301 TGGCCAAAGACACTGCCTTCCTGGGCATCACAGATGAGGCACCCGAAGGCCAGTTCATGT 242

Qy  590 ATCTGACAGGAAATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTG 649
            | |||| ||||||||  |||| |||||||||||||| | || || ||||||  ||||
Db  241 ACGTGACGGGCGGAGGTGACCTGACCTACGACCTCTACCAACTGGAAGAAGGATGAGCCAAATGACCACG 182

Qy  650 GTTCTGATGAAGATTGTGTATTGCTACTGAAAAATGCCAGTGAATGACGTCCCCTGCT 709
            ||| ||| ||||| |||| |  | ||| || |||| ||||||||||| | |||||||
Db  181 GTTCAGGGGAGGACTGTGTGATTCTCCTGACAATGGGCTCTGGAATGACATCTCCTGCA 122

Qy  710 CCACCTCCCCATCGGCCGTCTGGTCAGTTCCCTATCTGA 747
            || | ||||||||| |||||||||||||| | | |||
Db  121 CGGCCTCCTACATCGCCGTCTGTGGAGTTTCCTGCCTGA 84
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RESULT 10

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AV660023
AV660023
LOCUS      AV660023    367 bp   mRNA   linear   EST 16-JAN-2002
DEFINITION AV660023 GLC Homo sapiens cDNA clone GLCGDC05 3', mRNA sequence.
ACCESSION  AV660023
VERSION    AV660023.1  GI:9881037
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 367)
  AUTHORS  Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
           Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
           Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
           Hu,G., Gu,J., Chen,Z. and Han,Z.
  TITLE    Insight into hepatocellular carcinogenesis at transcriptome level
           by comparing gene expression profiles of hepatocellular carcinoma
           with those of corresponding noncancerous liver
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334 AGAAAGCTCTGCAAACAGAAATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCGGGC 393
        ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
297 ATTGCAGCCCTACGATCAGAGCTGAGAGCCCTGAGAAACTGGGTGCTCTTCTCTGAGT 356

394 AAACAAGTTGGGAACAAGTTCTTCTGACCAATGGTGAAATAATGACCTTTGAAAAAGTG 453
        ||   ||||||| ||||||||| |||| | ||| ||||||||| ||  ||||||||
357 GAAAAAGTTGGAAGAAG-TATTTGTGAGCAGTGTTAAAAAGATGAGCCCTTGACAGAGTG 415

454 AAGGCCTTGTGTGTCAGGCCTTCTGTGTGCCACCCCCAGGAATGCTGCAGAGAAT 513
        ||||||||| ||||||||||||||||||||||||||| |||||||||||||||||
416 AAGGCCCGTGTCCGAATTCCAGG-CTCTGTGCCACTCCCAGGAATGCTGAGGAAAC 474

514 GGAGCCATTCATCATCAAGGAGAAGCCTTCTCTGGGCATCACTGATGATGAGAGACA 573
        ||||| ||||| | |||||| || |||||||||||||||| ||||||||| |||||
475 TCGGCCATCCATCCAAAGAATGCTGGCCAAGATATTGCTGGGCATCACAGATGTGAGGGTT 534

574 GAAGGGCAGTTTGTGTTCTGATGAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGG 633
        |||| | || ||| ||||||||| ||||||||| |||| ||||||||||| ||||||
535 GAAGGCCAGTTTTTGAGGATTCGACAGGAAACAGAGTGCGCTATACTAATTGGAATGATGGG 594

634 GAACCCAACAATGCTGCTTCTGATGAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGG 693
        ||||||||||| | || |||  |  ||| || ||| |  | ||| || |||| |||
595 GAGCCCAACACACGGGCCGATGGGAAGACTGCTGTGTGTGATCTTGGGAAATGCCAAGTGG 654

694 AATGAGTCCCT-GCTCCACCTCCCCATCGGCCGTCTGGTCAGTTCCCTATCTGA 747
        || | ||| |  ||||  ||| |||| | | | ||||||||||||||||||||
655 AACGATGTCCCCTGGCTCTTTTTGGCAATCTGTTGAATTCTGTGACTGA 709
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RESULT 9

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CK778513/c
LOCUS      CK778513    722 bp   mRNA   linear   EST 20-FEB-2004
DEFINITION 965575 MARC 3BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION  CK778513
VERSION    CK778513.1  GI:42730826
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
  ORGANISM Bos taurus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
           Bovinae; Bos.
REFERENCE  1  (bases 1 to 722)
  AUTHORS  Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
           Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
           Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
           Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
           Quackenbush,J. and Keele,J.W.
  TITLE    Sequence evaluation of four pooled-tissue normalized bovine cDNA
           libraries and construction of a gene index for cattle
  JOURNAL  Genome Res. 11 (4), 626-630 (2001)
  MEDLINE  21180013
   PUBMED  11282978
COMMENT    Contact: Smith TPL
           USDA, ARS, US Meat Animal Research Center
           PO Box 166, Clay Center, NE 68933-0166, USA
           Tel: 402 762 4366
           Fax: 402 762 4390
           Email: smith@email.marc.usda.gov
           Single pass sequencing. Bases called with phred v0.020425.c and
           trimmed with the aid of the trim_alt option. Vector identified with
           cross_match v0.990329.
           Plate: 66 row: E column: 1
           Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
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                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 3BOV"
                     /note="vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
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JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE   21625106
PUBMED   11752456
COMMENT   Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.

FEATURES   Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="GLCGDC05"
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                /dev_stage="Adult"
                /lab_host="SOLR"
                /clone_lib="GLC"
                /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                XhoI"

ORIGIN

Query Match   40.6%;   Score 303; DB 1; Length 367;
Best Local Similarity 87.2%;   Pred. No. 2.6e-75;
Matches 367;   Conservative   0;   Mismatches   0;   Indels 54; Gaps   1;

Qy   174 AAAGGGGGAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCCTGGAAAGTTGGGGCC 233
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Db   1 AAAGGGGGAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCCTGGAAAGTTGGGGCC 60

Qy   234 TCCAGGAAATCCAGGGCCCTTCTGGGTCACCAGGACCAAAAAGGAGACCCTGG 293
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCCAGGAAATCCAGGGCCCTTCTGGGTCACCAGGACCAAAAAGGAGACCCTGG 120

Qy   294 AAAAAGTCCGGATGGTGATAGTAGTCCTGGCTGCCTCAGAAGAAAAGCTCTGCAAACAGA 353
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AAAAAGTCCGGATGGTGATAGTAGTCCTGGCTGCCTCAGAAGAAAAGCTCTGCAAACAGA 180

Qy   354 AATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGGTCAAACAAGTTGGGAACAAGTT 413
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGGTCAAACAAGTTGGGAACAAGTT 240

Qy   414 CTTCCTGACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTT 473
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Db   241 CTTCCTGACCAATGGTGAAATAATGACCTTTG----------------------------- 272

Qy   474 CCAGGCCTCGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAAATTCTCAT 533
                                             ||||||||||||||||||||||||||||
Db   273 -------------------------------ATGCTGCAGAGAATGGAGCCATTCAGAAATTCTCAT 306

Qy   534 CAAGGAGGAAGCCCTTCCTGGCATCACTGATGAGAAGAAGACAGAGAGGGCAGTTTGTGGATCT 593
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   307 CAAGGAGGAAGCCCTTCCTGGCATCACTGATGAGAAGAAGACAGAGAGGGCAGTTTGTGGATCT 366

Qy   594 G 594

Db   367 G 367

RESULT 11
AI255533
LOCUS   AI255533   657 bp   mRNA   linear   EST 12-NOV-1998
DEFINITION ui55f12.y1 Sugano mouse liver mlia Mus musculus cDNA clone
            IMAGE:1886351 5' similar to gb:DI1440 Mouse mRNA for P28a subunit
            of Ra-reactive factor, complete (MOUSE);, mRNA sequence.
ACCESSION   AI255533
VERSION   AI255533.1   GI:3863058
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 657)
REFERENCE
AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
           Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
           Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
           Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
           Waterston,R.
TITLE   The WashU-HHMI Mouse EST Project
JOURNAL   Unpublished (1996)
COMMENT   Contact: Marra M/Mouse EST Project
           WashU-HHMI Mouse EST Project
           Washington University School of MedicineP
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: mouseest@watson.wustl.edu
           This clone is available royalty-free through LLNL ; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           MGI:970675
           Seq primer: custom primer used
           High quality sequence stop: 488.

FEATURES   Location/Qualifiers
     source   1..657
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL"
                /db_xref="taxon:10090"
                /clone="IMAGE:1886351"
                /sex="female"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="Sugano mouse liver mlia"
                /note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
                (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                was primed with an oligo(dT) primer
                [ATGTGCGCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
                and cloned into distinct DraIII sites of the pME18S-FL3
                vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
                be used to isolate the cDNA insert. Size selection was
                performed to exclude fragments <1.5kb. Library
                constructed by Dr. Sumio Sugano (University of Tokyo
                Institute of Medical Science). Custom primers for
                sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                primer CGACCTGCAGCTCGAGCACA."

ORIGIN

Query Match   40.5%;   Score 302.2; DB 1; Length 657;
Best Local Similarity 71.5%;   Pred. No. 5.4e-75;
Matches 397;   Conservative   0;   Mismatches 158;   Indels   0;   Gaps   0;

Qy   101 CAGTGATTGCCTGTAGCTCTCAGGCATCAACGGCTTCCAGGCAAAGATGGGCGTGATG 160
             ||||||| ||||||| |||||||||||||||||||||||||||||| |||||||||
Db   19 CTGTGGTTACCTGCAGTTCTCGAGGCTCGATGGCTTCCAGGCAAAGATGGCGACGTGACG 78

Qy   161 GCACCAAGGAGGAAGAAAAGGGGAACCAGGCCAAGGGCTTACAGGGCCCCCTG 220
             | |||||||||||||||||||||||||||||| |||| ||||||||||||||||
Db   79 GTGCCAAGGAGGAAAAAGGGAGAACCAGGTCAAGGGCTTGCAAGGCCTTGCAAGGGCCCCTTCCTG 138

Qy   221 GAAAGTTGGGGCCTTCCAGGAAATCCAGGGCCTTCTCGGGTCACCAGGACCAAAGGGCCAAA 280
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Db   139 GAAAAGTAGGAGACCTTACAGGAGACCCCCGGGGTTAAAAGGAGCAGTGGGACCGA 198

Qy   281 AAGGAGACCCTGAAAAAGTCCGGATGGTGATAGTGTGATGATAGTGGCGTGATG 340
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Db   199 AAGGAGACCGTGGGGACAGAGGACAGAGAATTGATCTACTAGCGAAATTGATTCAGAAATTCAG 258

Qy   341 CTCTGCAAACAGAAATGCCACGTATCAAAAAGTGGCTGACCTTCTCTCTCTGGGCAAACAAG 400
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   259 CCCTACGATCAGAGCTGAGAGCCCTGAGAAACTGGGTGCTCTTCTCTCTGAGTGAAAAG 318

Qy   401 TTGGGAACAAGTTCTTCCTGACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCT 460

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Db   125 GCATCACGGCTTCCCAGGCGGTCAAAGATGGCGGTCGTGATGGCACCAGGGAGAAAGGGGGAAC 184
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Qy   153 GCCTGACGGCTTCCCAGGCAGGTCAAAGATGGCCAAGGGAGAAAAGGGAGAGAAGGGAGAC 212

Db   185 CAGGCCAAGGGCTCAGAGGCTTACGGCCACCCCCTGGAAAGTTGGGCGCCTGCGCGGGCCCC 244
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Qy   213 CGGGTCAAGGCCTGCAGAGGCTTGCCAGGGCATGCTGGAAAAAGGACCCTGCGAGGGCCCC 272

Db   245 CAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGAAAAGTCCGG 304
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Qy   273 CAGGGAATCTGGGTCAAAGGTGAGAGAAGGAGCAACCGGACCAAAAGGACCAAAGGTAG 332

Db   305 ATGGTGATAGTAGCCTGCCTCAGAAAGAAAAGCTCTGCAACAGGGAACAAGTTCTTCCTGACCA 364
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Qy   333 AATTTGATACTACCAACATTGATTTAGAAATTGCAGCCCTGCGATCGGAGCTCGAGAGCTA 392

Db   365 TCAAAAGTGGCTGACCTTCTCTTCATGAGTGAAAATGTTGGAAAGAAGTACTTCATGAGCA 424
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Qy   393 TGAGAAAGTGGGTGCTCCTTCTTCTCATGAGTGAAAAAGTGAAGGCCTTGTGTCCAGGCCTCTG 484

Db   425 ATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTCCAGGCCTCTG 484
         || ||||||||| |||||||||||||||| |||||||||||||||||||||||
Qy   453 GTGTTAGAAGGATGCCCCTTAACAGAGGCGAAGGCTCTGTCCGCAACTCCAGGGCACTG 512

Db   485 TGGCCACCCCAGGAATGCGTCGAGAGCTGAGCGGATGAAATAGGGCCATCCAGAATTCTCATCAAGGAGAAG 544
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Qy   513 TGGCCACTCCCAGGAATGCTGAGGAAATAGCTGAGGAAAATAGGGCCATCCAGAATGTGCCAAAGATGTTG 572

Db   545 CCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCCAGTTGTTGTGGATCGGAAAATA 604
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Qy   573 CCTTCTTGGGCATAACCGAGGACCTGAAAACGTTTTTGAGGAGGACCTGACAGGAAACA 632

Db   605 GACTGACCTACACAAACTGGAACGAGGG 632
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Qy   633 GAGTGCGCTACACTAACTGGAATGAGGG 660
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RESULT 13
AY325178

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LOCUS       AY325178              1162 bp    mRNA    linear   HTC 26-JUL-2003
DEFINITION  Rattus norvegicus Ab2-001 mRNA, complete cds.
ACCESSION   AY325178
VERSION     AY325178.1  GI:33086533
KEYWORDS    HTC.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 1162)
  AUTHORS   Xu,C.S., Li,W.Q., Li,Y.C., Ma,H., Wang,L., Wang,S.F., Han,H.P.,
            Wang,G.P., Chai,L.Q., Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F.,
            Zhao,L.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
  TITLE     Liver regeneration after PH
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1162)
  AUTHORS   Xu,C.S., Li,W.Q., Li,Y.C., Ma,H., Wang,L., Wang,S.F., Han,H.P.,
            Wang,G.P., Chai,L.Q., Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F.,
            Zhao,L.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUN-2003) Henan Bioengineering Key Lab, Henan Normal
            University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
            China
FEATURES             Location/Qualifiers
     source          1..1162
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                     /db_xref="taxon:10116"
     CDS             41..1156
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                     /product="Ab2-001"
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RESULT 12
AY325174

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LOCUS       AY325174              1162 bp    mRNA    linear   HTC 26-JUL-2003
DEFINITION  Rattus norvegicus Ab2-011 mRNA, complete cds.
ACCESSION   AY325174
VERSION     AY325174.1  GI:33086525
KEYWORDS    HTC.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 1162)
  AUTHORS   Xu,C.S., Li,W.Q., Li,Y.C., Han,H.P., Wang,G.P., Chai,L.Q.,
            Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H.,
            Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
  TITLE     Liver regeneration after PH
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1162)
  AUTHORS   Xu,C.S., Li,W.Q., Li,Y.C., Han,H.P., Wang,G.P., Chai,L.Q.,
            Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H.,
            Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUN-2003) Henan Bioengineering Key Lab, Henan Normal
            University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
            China
FEATURES             Location/Qualifiers
     source          1..1162
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                     /product="Ab2-011"
                     /protein_id="AAP92575.1"
                     /db_xref="GI:33086526"
                     /translation="MSLFTSFLLCVLTAVYAETLTEGAQSSCPVIACSSPGLNGFPG
                     KDGHDGAKGSKGEPGQGLRGLQGPPGKVGPAGPPGNPGSKGATGPKGDRGESVEFDTT
                     NIDLEIAALRSELRAMRKWTLLSMSENVGKKYFMSSVRRMPLNRAKALCSELQGTVAT
                     PRNAEENRAIQNVAKDVAPLGITDQRTENVFEDLTGNRVRYTNWNEGRLSLRGPELHG
                     PAANSVYTPSSSDTENIPPTEETAKDGCALDPYEQSLIHAATESKANSENQHYTLEK
                     QSVHISVSVSVEFLVNLQMFAVTVSSHITRGNRRSLTPGLTHEDFPHKQADSPSLELTG
                     WLDRMASEPAGCSGLPSCSTRIVDVCQVYLDTMTMFV"
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ORIGIN

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Query Match       40.3%;   Score 301.4;   DB 3;  Length 1162;
Best Local Similarity   70.6%;   Pred. No. 1.1e-74;
Matches   401;  Conservative   0;  Mismatches 167;  Indels   0;  Gaps   0;

Qy   65 CTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCCAGTGATTGCCTCAGTGATTGCCTCTCCAG 124
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/db_xref="GI:33086534"
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NIDLETAALRSELRAMRKWVLLSMSENVGKKYFMSSVRRMPLNRAKALCSELQGTVAT
PRNAEENRAIQNVAKDVAFLGITDQRTENVFEDLTGNRVRYTNWNEGRLSLRGPELHG
PAANSVVYTPSSSDTENIPPTBETAKDGCALLDPYEQSLIHAATESKANSENQHYTLEK
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ORIGIN

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Query Match        40.3%;    Score 301.4;  DB 3;    Length 1162;
Best Local Similarity  70.6%;   Pred. No. 1.1e-74;
Matches  401;   Conservative  0;   Mismatches  167;   Indels  0;   Gaps  0;

Qy   65 CTGTGACCTGAGGATGCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGTCTCCAG 124
           |||||||| |||||  |   ||||  || | || ||| || | |||  ||| ||||
Db   93 CCGAGACCTTAACCGAAGGGGCTCAAAGTAGCTGCCCTGTGATTGCCTGCAGTTCTCCGG 152

Qy  125 GCATCAACGGCTTCCCAGGCCAAAGATGGGCGTGATGGCCACCAAGGGAGAAAAGGGGAAC 184
           |||| ||| ||||||||||||| |||  |||||| |||  ||||  |||||||| |||||
Db  153 GCCTGAACGGCTTCCCAGGCCAAAGATGGGCAACGACGACGGTGCCAAGGGAGAAAAGGGAGAAC 212

Qy  185 CAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGCCTCCAGGAAATC 244
           | |||||||||||||||||||||| |||||||| | ||||  ||  |||||||| |
Db  213 CGGGTCAAGGGCTCAGAGGCTTGCAGGGCCCTCCTGGAAAGTAGGACCTGCAGGGCCCC 272

Qy  245 CAGGGCCCTTCTGGGTCACCAGGACCAAAGGCCAAAAGGCCAAAAAGAGAACCCTGGAAAAGTCCGG 304
           |||||| |||||||||| ||| |||  || ||||||||||| ||||||| ||||| ||||
Db  273 CAGGGAATCCTGGGTCAAAGGACCAACGGGACCAAAGGACCAAAGGAGACCGTGTAG 332

Qy  305 ATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCACGTA 364
           ||||| |  |||| || ||||| ||||| |||| | | |||   |||||||||
Db  333 AATTTGATACTACCAACATTGATTTAGAAATTGCAGCCCCTGCGATCGGAGCTGAGAGCTA 392

Qy  365 TCAAAAAGTGGCTGACCTTCTCTCTGGGCAACAAGTTGGAACAAGTTCTTCCTGACCA 424
           |  ||||| |||||||| |||||||||| |||||   |||||||||||| | ||
Db  393 TGAGAAAGTGGCTGCTCCTTTCTATGATGTGAAATGTTGGAAAGAAGTACTTCATGAGCA 452

Qy  425 ATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGCTCAAGTCTCCAGGCACTG 484
           |||||| |  |||  ||  | ||||||  ||||||| ||| |||| | |||||| |||
Db  453 GTGTTTAGAAGGATGCCCCCTTAACAGACGAAGGCTCTGTGTCGCTCCAGGGCACTG 512

Qy  485 TGGCCACCCCCAGGAAGTGCTGCGAGAATGCTGCGAGGAATGGAGCGATGGAGCCATTCAGAAT 544
           |||||||||||||||| | |||||||| |   ||||||  ||| | ||| | ||| |
Db  513 TGGCCACTCCCAGGAATGCTGAGGGAAATAGGGCCATTCCCAGAAATGTGGCCAAAGATGTTG 572

Qy  545 CCTTCCTGGGCATCACTGATGAGAAGACAGAGGGCAGTTTGGATCTGACAGGAAATA 604
           ||||||||||| ||||||||| | | | || | |||| |||||| || ||
Db  573 CCTTCTTGGGCATAACGGACTGAAAACGTTTTGAGGACCTGAAAACG 632

Qy  605 GACTGACCTACACAAACTGGAACGAGGG 632
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Db  633 GAGTGCGCTACACTAACTGGAATGGAGGG 660
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RESULT 14

AI195233/c

LOCUS   AI195233   869 bp   mRNA   linear   EST 14-OCT-1998
DEFINITION ui62c03.x1 Sugano mouse liver mlia Mus musculus cDNA clone
            IMAGE:1886980 3' similar to gb:X15422_cds1 MANNOSE-BINDING PROTEIN
            C PRECURSOR (HUMAN) ; gb:D11440 Mouse mRNA for P28a subunit of
            Ra-reactive factor, complete (MOUSE);, mRNA sequence.
ACCESSION   AI195233
VERSION   AI195233.1   GI:3747839
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 869)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,P., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE   The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
  COMMENT   Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:971304
            Seq primer: custom primer used
            High quality sequence stop: 428.

FEATURES   Location/Qualifiers
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                     /clone="IMAGE:1886980"
                     /sex="female"
                     /dev_stage="adult"
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                     /clone_lib="Sugano mouse liver mlia"
                     /note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
                     (CACTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
                     ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
                     and cloned into distinct DraIII sites of the pME18S-FL3
                     vector (5' site CACTGTG, 3' site CACCATGTG). XhoI should
                     be used to isolate the cDNA insert. Size selection was
                     performed to exclude fragments <1.5kb. Library
                     constructed by Dr. Sumio Sugano (University of Tokyo
                     Institute of Medical Science). Custom primers for
                     sequencing: 5' end primer CTTCGCTCTAAAAGCTGCG and 3' end
                     primer CGACCTGCAGCTCGAGCACA."

ORIGIN

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Query Match        39.1%;    Score 292.4;  DB 1;    Length 869;
Best Local Similarity  67.0%;   Pred. No. 3.8e-72;
Matches  424;   Conservative  0;   Mismatches  208;   Indels  1;   Gaps  1;

Qy  115 AGCTCTCCAGGCATCAACGGCTTCCCAGGCCAAAGATGGGCGTGATGGCCACCAAGGGAGAA 174
           |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db  805 AGTTCTCCAAGGCCTGAATGCCTACCNAGCAAAGATGGGACGTNACGGTCAAAGGGAGAA 746

Qy  175 AAGGGGAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCT 234
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Qy  235 CCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGTTAAAGGTACCGTACCGGAG 294
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Db  685 TACAGGACCCNCAGGGAATCCGGGGTTAAAGGAGCAGTAGTGTACCGTACCGAAAGGTCNG 626

Qy  295 AAAAGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAA 354
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Db  625 GACAGAGCAGAATTTGATACTACCAACATTGATTGATCAGAAATTGCAGCCCCTACGATCAGAG 566

Qy  355 ATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAACAAGTTGGGAACAAGTTC 414
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Qy  415 TTCCTGACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTTCAAGTTC 474
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Qy  475 CAGGCCCTGTGTGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATC 534
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Db   61 TCCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAGGGACCAAGAGGAGACCCTGG 120
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Qy  294 AAAAGTCCGATGGTGAGTAGTAGTCCTGCTGCTGCTGGGCAGTTTGTGGATCTG 353
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Qy  354 AATGGCAGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTT 413
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Db  181 ACAGGAAACAGAGTGCGCTATACTAATTGGAATGATGGGGAGCCCAACAACGGGGCGAT 267

Qy  414 CTTCCTGACCAATGGTGAAAAATGAGCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTT 473
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Db  241 CTTCCTGACCAATGGTGAAATAATGACCTTTG-------------------------- 272

Qy  474 CCAGGCCTCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCAT 533
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Db  273 ------------------------ATGCTGCAGAGAATGGAGCCATTCAGAATCTCAT 306

Qy  534 CAAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAGGGCAGTTTGTGGATCT 593
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Qy  594 G 594
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Search completed: June 20, 2005, 18:00:16
Job time : 3230 secs

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Db  446 CAGGGCCTCTGTGGCCACTCCCAGGAATGCTGAGGAAAACTCGGCCATCCAGAAAGTGGCC 387
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RESULT 15
AV660367

LOCUS	AV660367 367 bp mRNA linear EST 16-JAN-2002
DEFINITION	AV660367 GLC Homo sapiens cDNA clone GLCGGH07 3', mRNA sequence.
ACCESSION	AV660367
VERSION	AV660367.1 GI:9881381
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 367)
AUTHORS	Xu,X., Huang,J., Xu,J., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
	Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
	Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
	Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE	Insight into hepatocellular carcinogenesis at transcriptome level
	by comparing gene expression profiles of hepatocellular carcinoma
	with those of corresponding noncancerous liver
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE	21625106
PUBMED	11752456
COMMENT	Contact: Zeguang Han
	Chinese National Human Genome Center at Shanghai
	351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
	201203, P. R. China
	Tel: 86-21-50801919(ex.45)
	Fax: 86-21-50801922
	Email: hanzg@chgc.sh.cn
	This clone is available at CHGC in Shanghai.
FEATURES	Location/Qualifiers
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	/dev_stage="Adult"
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	/clone_lib="GLC"
	/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"
ORIGIN	

Query Match   39.0%;   Score 291; DB 1; Length 367;
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Matches 366; Conservative   0; Mismatches   0; Indels 55; Gaps   2;

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Qy  174 AAAGGGGGAACCAGGCCAAGGGCTTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCC 233
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Db    1 AAAGGGGAACCAGGCCAAGGGCTTACAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCC 60
Qy  234 TCCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAGAGGAGACCCTGG 293
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